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OM protein - protein search, using SW model										
Run on: May 15, 2006, 16:53:57 ; Search time 145.923 seconds (without alignments)										
376.380 Million cell updates/sec										
Title: US-10-041-860-48										
Perfect score: 672										
Sequence: 1 QVQLVQSGRAEVKRGASVKGKVVV.....YDYYGMDVWGQCTTVTVSS 125										
Scoring table: BLOSUM62										
Gapop 10.0 , Gapext 0.5										
Searched: 2443163 seqs, 4393781 residues										
Total number of hits satisfying chosen parameters:	2443163									
Minimum DB seq length: 0										
Maximum DB seq length: 2000000000										
Post-processing: Minimum Match 0%										
Listing first 45 summaries										
Database : A_Geneseq_21:*										
1: geneseq21900s:*										
2: Geneseq21900s:*										
3: Geneseq2000s:*										
4: geneseq2001s:*										
5: Geneseq2002s:*										
6: Geneseq2003as:*										
7: geneseq2003bs:*										
8: Geneseq2004s:*										
9: Geneseq2005s:*										
Post-processing: Minimum Match 0%										
Listing first 45 summaries										
Result No. Score Query Match Length DB ID Description										
1 672 100.0 125 7 ADK18776 Anti-huma										
2 672 100.0 125 7 ADK18948 Anti-huma										
3 672 100.0 125 7 ADK18624 Anti-huma										
4 672 100.0 125 8 ADK18813 Anti-huma										
5 672 100.0 125 8 ADK125392 Human mAb										
6 638 94.9 125 7 ADK18614 Anti-huma										
7 638 94.9 125 7 ADK18779 Anti-huma										
8 638 94.9 125 7 ADK18919 Anti-huma										
9 638 94.9 125 7 ADK18816 Anti-huma										
10 638 94.9 125 8 ADK125448 Human mAb										
11 593.5 88.3 126 7 ADK18864 Anti-huma										
12 593.5 88.3 126 7 ADK18595 Anti-huma										
13 593.5 88.3 126 7 ADK18777 Anti-huma										
14 593.5 88.3 126 8 ADK125408 Human mAb										
15 579.5 86.2 125 7 ADK18814 Anti-huma										
16 575.5 85.6 126 7 ADK18925 Anti-huma										
17 575.5 85.6 126 7 ADK18780 Anti-huma										
18 575.5 85.6 126 7 ADK18616 Anti-huma										
19 575.5 85.6 126 7 ADK18817 Anti-huma										
20 575.5 85.6 126 8 ADK125448 Human mAb										
21 572 85.1 127 7 ADK18620 Anti-huma										
22 572 85.1 127 7 ADK18818 Anti-huma										
23 572 85.1 127 7 ADK18781 Anti-huma										
24 572 85.1 127 7 ADK18936 Anti-huma										

ALIGNMENTS

RESULT 1	ADK18776	ID	ADK18776	standard; protein; 125 AA.
		XX	ADK18776;	
		AC		
		XX		
		DT	06-MAY-2004 (first entry)	
		XX		
		DS	Anti-human PDGF-D antibody protein related sequence #2.	
		XX		
		KW	antiinflammatory; immunomodulator; cytostatic; gene therapy.	
		XX		
		OS	Homo sapiens.	
		XX		
		PN	WO2003057857-A2.	
		XX		
		PR	07-JAN-2002; 2002US-00041860.	
		XX		
		PA	(ABGENIX INC.	
		PI	Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazzit G, Weber R;	
		PI	Bezzabeh B;	
		XX		
		DR	WPI; 2003-587119/55.	
		XX		
		PT	New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.	
		PT	SBQ ID NO 200; 255pp; English.	
		PS	Disclosure; SBQ ID NO 200; 255pp; English.	
		CC	The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to Platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 3064188.0.99 arising in the conditioned medium obtained when HEK233 cells are transfected with the plasmid pCPBP4/Sec-3064188. This sequence corresponds to a protein used in the invention.	
		CC	Sequence 125 AA;	

RESULT 4
ADK18813
ID ADK18813 standard; protein; 125 AA.
XX ADK18813;
AC ADK18813;
XX 05-MAY-2004 (first entry)
DT Anti-human PDGF-D antibody protein related sequence #39.
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX Homo sapiens.
OS Homo sapiens.
XX WO2003057857-A2.
XX PD 17-JUL-2003.
XX PP 06-JAN-2003; 2003WO-US000398.
PR 07-JAN-2002; 2002US-00041860.
PA (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R,
PI Bezabeh B;
XX DR 2003-587119/55.
PT New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
PS Disclosure; SEQ ID NO 237; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 3066188.0.99 arising in the conditioned medium obtained when HK293 cells are transfected with the plasmid PCBP/Sec-3066188. This sequence corresponds to a protein used in the invention.
XX Sequence 125 AA;
Qy 1 QYLVQSGAEVKPGASVKSCKASGYFTSYDINWVQATQGLEWMGWINPNSNTDY 60
Db 1 QYLVQSGAEVKPGASVKSCKASGYFTSYDINWVQATQGLEWMGWINPNSNTDY 60
Qy 61 AQKPGQGRVMTMRTDTISSTAYMELSSRLRSEDTAIYYCYRGFCYSYNDYYCQMDVNCQGTT 120
Db 61 AQKPGQGRVMTMRTDTISSTAYMELSSRLRSEDTAIYYCYRGFCYSYNDYYCQMDVNCQGTT 120
Qy 121 VTVSS 125
Db 121 VTVSS 125

Query Match 100.0%; Score 672; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 3e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QYLVQSGAEVKPGASVKSCKASGYFTSYDINWVQATQGLEWMGWINPNSNTDY 60
Db 1 QYLVQSGAEVKPGASVKSCKASGYFTSYDINWVQATQGLEWMGWINPNSNTDY 60
Qy 61 AQKPGQGRVMTMRTDTISSTAYMELSSRLRSEDTAIYYCYRGFCYSYNDYYCQMDVNCQGTT 120
Db 61 AQKPGQGRVMTMRTDTISSTAYMELSSRLRSEDTAIYYCYRGFCYSYNDYYCQMDVNCQGTT 120
Qy 121 VTVSS 125
Db 121 VTVSS 125

RESULT 5
ADL25392
ID ADL25392 standard; protein; 125 AA.
XX ADL25392;
AC ADK18614;
XX

Query Match 100.0%; Score 672; DB 8; Length 125;
Best Local Similarity 100.0%; Pred. No. 3e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QYLVQSGAEVKPGASVKSCKASGYFTSYDINWVQATQGLEWMGWINPNSNTDY 60
Db 1 QYLVQSGAEVKPGASVKSCKASGYFTSYDINWVQATQGLEWMGWINPNSNTDY 60
Qy 61 AQKPGQGRVMTMRTDTISSTAYMELSSRLRSEDTAIYYCYRGFCYSYNDYYCQMDVNCQGTT 120
Db 61 AQKPGQGRVMTMRTDTISSTAYMELSSRLRSEDTAIYYCYRGFCYSYNDYYCQMDVNCQGTT 120
Qy 121 VTVSS 125
Db 121 VTVSS 125

RESULT 6
ADK18614
ID ADK18614 standard; protein; 125 AA.
XX ADK18614;
AC ADK18614;
XX

DT	06-MAY-2004	(first entry)	PN	WO2003057857-A2.
XX	Anti-human PDGF-D antibody heavy chain protein sequence.	XX	XX	XX
XX	anti-inflammatory; immunomodulator; cytostatic; gene therapy.	XX	XX	XX
XX	Homo sapiens.	XX	XX	XX
XX	WO2003057857-A2.	XX	XX	XX
XX	17-JUL-2003.	XX	XX	XX
XX	06-JAN-2003; 2003WO-US000398.	XX	XX	XX
XX	07-JAN-2002; 2002US-00041860.	XX	XX	XX
XX	(ABGEN-) ABGENIX INC.	XX	XX	XX
XX	Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R; Bezabeh B;	XX	XX	XX
XX	WPI; 2003-587119/55.	XX	XX	XX
XX	New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.	XX	XX	XX
XX	Disclosure; SEQ ID NO 38; 255pp; English.	XX	XX	XX
XX	The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.	CC	CC	CC
XX	Sequence 125 AA;	CC	CC	CC
XX	Query Match 94.9%; Score 638; DB 7; Length 125; Best Local Similarity 94.4%; Pred. No. 4.2e-51; Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0	CC	CC	CC
XX	Qy 1 QVQLVQSGAEVYKPKGASVKSCKASYYTFSYDINVRQATGQLEWMGWINPNSGNTDY 60 Db 1 QVQLVQSGAEVYKPKGASVKSCKASYYTFSYDINVRQATGQLEWMGWINPNSGNTGY 60	CC	CC	CC
XX	Sequence 125 AA;	CC	CC	CC
XX	Query Match 94.9%; Score 638; DB 7; Length 125; Best Local Similarity 94.4%; Pred. No. 4.2e-51; Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0	CC	CC	CC
XX	Qy 1 QVQLVQSGAEVYKPKGASVKSCKASYYTFSYDINVRQATGQLEWMGWINPNSGNTGY 60 Db 1 QVQLVQSGAEVYKPKGASVKSCKASYYTFSYDINVRQATGQLEWMGWINPNSGNTGY 60	CC	CC	CC
XX	RESULT 8	CC	CC	CC
XX	ADK18919 standard; protein; 125 AA.	CC	CC	CC
XX	ADK18919;	CC	CC	CC
XX	06-MAY-2004 (first entry)	DT	DT	XX
XX	Anti-human PDGF-D antibody protein related sequence #145.	DB	DB	XX
XX	anti-inflammatory; immunomodulator; cytostatic; gene therapy.	XX	XX	XX
XX	Homo sapiens.	OS	OS	OS
XX	ADK18779;	XX	XX	XX
XX	06-MAY-2004 (first entry)	DT	DT	XX
XX	Anti-human PDGF-D antibody protein related sequence #5.	DB	DB	XX
XX	anti-inflammatory; immunomodulator; cytostatic; gene therapy.	XX	XX	XX
XX	Homo sapiens.	OS	OS	OS

(ABGE-) ABGENIX INC.
 XX Corvalan JRF; Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R,
 PI Bezabeh B,
 XX WPI; 2003-587119/55.

PT New human monoclonal antibody that binds to platelet-derived growth
 factor-D (PDGF-D), useful for treating chronic and recurrent human
 diseases, such as inflammation, autoimmunity and cancer.
 PR Disclosure; SEQ ID NO 343; 255pp; English.

CC The invention relates to a human monoclonal antibody that binds to
 platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 treating chronic and recurrent human diseases, such as inflammation,
 autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 useful for modulating collagen formation, and for staging various
 cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 generated using an active protein fragment of the gene product from the
 clone 30664188.0.99 arising in the conditioned medium obtained when
 HEK293 cells are transfected with the plasmid PCEP4/Sec-30664188. This
 sequence corresponds to a protein used in the invention.
 XX Sequence 125 AA;

Query Match 94.9%; Score 638; DB 7; Length 125;
 Best Local Similarity 94.4%; Pred. No. 4.2e-51;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 SQ Sequence 125 AA;

Qy 1 QYLVQSGAEVKPGASVKSCASGTTSYDINWRAOTQGLEMGWNPNSGNTDY 60
 Db 1 QYLVQSGAEVKPGASVKSCASGTTSYDINWRAOTQGLEMGWNPNSGNTGY 60

RESULT 10
 ADL2544 standard; protein; 125 AA.
 XX DT 17-JUN-2004 (first entry)

Human mAb 1.45 heavy chain variable region protein SEQ ID NO:54.
 XX DE ADL2544;
 XX AC ADL2544;
 XX DT 17-JUN-2004 (first entry)

Human mAb 1.45 heavy chain variable region protein SEQ ID NO:54.
 XX DE ADL2544;
 XX AC ADL2544;
 XX DT 06-MAY-2004 (first entry)

Anti-human PDGF-D antibody protein related sequence #42.
 XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX OS Homo sapiens.
 XX PN WO2003057857-A2.
 XX PR 17-JUL-2003.
 XX PF 06-JAN-2003; 2003WO-US000398.

RESULT 9
 ADK18816
 ID ADK18816 standard; protein; 125 AA.
 XX AC ADK18816;
 XX DT 06-MAY-2004 (first entry)

Anti-human PDGF-D antibody protein related sequence #42.
 XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX OS Homo sapiens.
 XX PN WO2003057857-A2.
 XX PR 17-JUL-2003.
 XX PF 06-JAN-2003; 2003WO-US000398.

(ABGE-) ABGENIX INC.
 XX Corvalan JRF; Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R,
 PI Bezabeh B,
 XX WPI; 2003-587119/55.

PT New human monoclonal antibody that binds to platelet-derived growth
 XX PR growth factor-DD (PDGF-DD) for preparing a medicament for treating
 PT PT nephritis.

PT Disclosure; SEQ ID NO 240; 255pp; English.

CC The invention relates to a human monoclonal antibody that binds to
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 30664188.0.99 arising in the conditioned medium obtained when
 CC HEK293 cells are transfected with the plasmid PCEP4/Sec-30664188. This
 CC sequence corresponds to a protein used in the invention.
 XX Sequence 125 AA;

Query Match 94.9%; Score 638; DB 7; Length 125;
 Best Local Similarity 94.4%; Pred. No. 4.2e-51;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 SQ Sequence 125 AA;

Qy 1 QYLVQSGAEVKPGASVKSCASGTTSYDINWRAOTQGLEMGWNPNSGNTDY 60
 Db 1 QYLVQSGAEVKPGASVKSCASGTTSYDINWRAOTQGLEMGWNPNSGNTGY 60

RESULT 10
 ADL2544 standard; protein; 125 AA.
 XX DT 17-JUN-2004 (first entry)

Human mAb 1.45 heavy chain variable region protein SEQ ID NO:54.
 XX DE ADL2544;
 XX AC ADL2544;
 XX DT 17-JUN-2004 (first entry)

Human mAb 1.45 heavy chain variable region protein SEQ ID NO:54.
 XX DE ADL2544;
 XX AC ADL2544;
 XX DT 06-MAY-2004 (first entry)

Anti-human PDGF-D antibody protein related sequence #42.
 XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX OS Homo sapiens.
 XX PN WO2004024098-A2.
 XX PR 16-SEP-2003; 2003WO-US039414.
 XX PF 16-SEP-2003; 2002US-0411137P.

(ABGE-) ABGENIX INC.
 XX (ABGE-) ABGENIX INC.
 XX (CURA-) CURAGEN CORP.
 XX PI Floege J, Gazit-Bornstein G, Keyt B, Larchelle WJ, Lichenstein H;
 XX DR 2004-269881/25.
 XX DR N-PSDB; ADL25443.
 XX Use of an antibody or its binding fragment that binds platelet derived
 PT growth factor-DD (PDGF-DD) for preparing a medicament for treating
 PT nephritis.

PS Disclosure; SEQ ID NO 54; 115pp; English.

XX The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-**DD** (PDGF-**DD**), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antinflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-**DD**, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the exemplification of the present invention.

XX Sequence 125 AA;

Query Match 94.9%; Score 638; DB 8; Length 125;
Best Local Similarity 94.4%; Pred. No. 4.2e-51;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEYRKPGASVKVSKASGYTFSYDINVRQATGQGLEMMGWTNPNSGNTDY 60
Db 1 QVQLVQSGAEYRKPGASVKVSKASGYTFSYDINVRQATGQGLEMMGWTNPNSGNTDY 60

Qy 61 AQKFGQRTMTRDTISIATMELSSRSEDTAVYCARGSSSYSGDYXTGMDVNGQGTT 120
Db 61 AQKFGQRTMTRDTISIATMELSSRSEDTAVYCARGSSSYSGDYXTGMDVNGQGTT 120

Qy 121 VTIVSS 125
Db 121 VTIVSS 125

RESULT 12
ID ADK18595 standard; protein; 126 AA.
XX ADK18595;
AC ADK18595;
XX 06-MAY-2004 (first entry)

RESULT 11
ID ADK18864
ID ADK18864 standard; protein; 126 AA.
XX AC ADK18864;
XX DT 06-MAY-2004 (first entry)
XX Anti-human PDGF-D antibody heavy chain protein sequence.
DB 06-MAY-2004 (first entry)
XX Anti-human PDGF-D antibody protein related sequence #90.
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
OS Homo sapiens.
XX WO2003057857-A2.
XX 17-JUL-2003.
XX 06-JAN-2003; 2003WO-US000398.
XX 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX DR 17-JUL-2003.
XX 06-JAN-2003; 2003WO-US000398.
XX PR 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX DR 2003-587119/55.
XX New human monoclonal antibody that binds to platelet-derived growth factor-**D** (PDGF-**D**), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

PS Disclosure; SEQ ID NO 19; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-**D** (PDGF-**D**). The antibody is useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-**D** nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-**D** (PDGF-**D**) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

PS Disclosure; SEQ ID NO 288; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-**D** (PDGF-**D**). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation.

SQ	Sequence 126 AA;	Db	1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGMNPNSGNTGY 60
	Query Match 88.3%; Score 593.5; DB 7; Length 126;	Qy	61 AQKFGQGRVTMTRDTISISTAYMELSSLRSEDTAIVYCVR-GFGYSNNYDYYGMDWQGQT 119
	Best Local Similarity 89.7%; Pred. No. 5.4e-47; Mismatches 4; Indels 1; Gaps 1;	Db	61 AQKFGQGRVTMTRDTISISTAYMELSSLRSEDTAIVYCVR-GFGYSNNYDYYGMDWQGQT 120
Qy	1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGMNPNSGNTGY 60	Qy	120 TTVVSS 125
Db	1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGMNPNSGNTGY 60	Db	121 TTVVSS 126
Qy	61 AQKFGQGRVTMTRDTISISTAYMELSSLRSEDTAIVYCVR-GFGYSNNYDYYGMDWQGQT 119	RESULT 14	
Db	61 AQKFGQGRVTMTRDTISISTAYMELSSLRSEDTAIVYCVR-GFGYSNNYDYYGMDWQGQT 120	ID	ADL25408 standard; protein; 126 AA.
Qy	120 TTVVSS 125	XX	XX
Db	121 TTVVSS 126	DT	17-JUN-2004 (first entry)
		XX	Human mAb 1.18 heavy chain variable region protein SEQ ID NO:18.
		DS	
		XX	
		KW	antibody; binding fragment; platelet derived growth factor- DD ; PDGF- DD ;
		XX	nephritis; mesangial cell proliferation inhibition;
		AC	mesangial proliferative glomerulonephritis; nephrotropic;
		XX	anti-inflammatory; dermatological; immunosuppressive; antidiabetic;
		DT	gene therapy; human; monoclonal antibody; mAb.
		XX	
		DE	
		OS	
		XX	
		XX	
		PN	
		XX	
		PD	
		XX	
		PP	
		XX	
		PR	
		XX	
		XX	
		PA	
		XX	
		PA	(ABGE-) AGENIX INC.
		PA	(CURA-) CURAGEN CORP.
		XX	
		PI	
		XX	
		XX	
		DR	
		DR	WPI: 2004-269081/25.
		XX	
		PT	
		PT	Use of an antibody or its binding fragment that binds platelet derived growth factor- DD (PDGF- DD) for preparing a medicament for treating nephritis.
		PT	
		XX	
		PS	
		XX	
		CC	The present invention describes an antibody or its binding fragment that binds platelet derived growth factor- DD (PDGF- DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described:
		CC	(1) a method of detecting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antifibrotic, immunosuppressive and antidiabetic activities and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF- DD , can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the exemplification of the present invention.
		CC	
		XX	
		CC	Sequence 126 AA;
		CC	Sequence 126 AA;
		CC	Query Match 88.3%; Score 593.5; DB 8; Length 126;
		CC	Best Local Similarity 89.7%; Pred. No. 5.4e-47; Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
		CC	Query 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINVRQATGQGLEWMGMNPNSGNTDY 60

Db 1 QVQLVQSGAEVYKPGASVKVSKASGYTFTSYDINWVRQATQGLEWMGMNPNSGNTGY 60
 Qy 61 AQKFQSRVTRTDTTS-STATYMEELSSRLSRSRDTAIVYCTV-GFGYSYNDYIYGMDWGQGT 119
 61 AQKFQSRVTRTDTTS-STATYMEELSSRLSRSRDTAIVYCTV-GFGYSYNDYIYGMDWGQGT 120
 Db 120 TVTVSS 125
 Qy 121 TVTVSS 126
 Db 121 TVTVSS 126

RESULT 15
 ADK18814
 ID ADK18814 standard; protein; 125 AA.
 XX
 AC ADK18814;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 Anti-human PDGF-D antibody protein related sequence #40.
 XX
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057857-A2.
 XX
 PD 17-JUL-2003.
 XX
 PP 06-JAN-2003; 2003WO-US000398.
 XX
 PR 07-JAN-2002; 2002US-00041860.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX
 DR WPI; 2003-587119/55.
 XX
 New human monoclonal antibody that binds to platelet-derived growth
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as, inflammation, autoimmunity and cancer.
 XX
 Disclosure; SEQ ID NO 238; 255bp; English.

XX
 The invention relates to a human monoclonal antibody that binds to
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 3066188_0_99 arising in the conditioned medium obtained when
 CC HEK293 cells are transfected with the plasmid PCBP4/Sec-3_0664188. This
 CC sequence corresponds to a protein used in the invention.
 XX
 SQ Sequence 125 AA;

Query Match 86.2%; Score 579.5; DB 7; Length 125;
 Best Local Similarity 89.4%; Pred. No. 1.1e-45;
 Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
 Qy 4 LVQSGAVKKEPGASVKVSKASGYTFTSYDINWVRQATQGLEWMGMNPNSGNTGYAQK 63
 3 LVQSGAVKKEPGASVKVSKASGYTFTSYDINWVRQATQGLEWMGMNPNSGNTGYAQK 62
 Db 64 FGGRVTRTDTTS-STATYMEELSSRLSRSRDTAIVYCTV-GFGYSYNDYIYGMDWGQGT 122
 Qy 63 FGGRVTRTDTTS-STATYMEELSSRLSRSRDTAIVYCTV-GREGIAVAGTYYYYGMDWGQGT 122
 Db 123 VSS 125
 Qy 123 VSS 125

Db 123 VSS 125
 Search completed: May 15, 2006, 16:58:54
 Job time : 146.923 secs

GenCore version 5.1.8
(c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 17:04:12 ; Search time 35.4077 Seconds

(without alignments)
291.870 Million cell updates/sec

Title: US-10-041-860-48

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKGASVRY.....YDYYGMDVWGQGTVTVSS 125

Scoring table: BLOSUM62

Gapext 0.5

Searched: 572060 seqs, 822675679 residues

Total number of hits satisfying chosen parameters:

572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:
 4: /cgn2_6/ptodata/1/iaa/PCTNS_COMB.pep:
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:
 6: /cgn2_6/ptodata/1/iaa/backfile/pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541.5	80.6	120	2 US-09-025-769B-36	Sequence 36, App1
2	541.5	80.6	120	2 US-09-025-769B-59	Sequence 59, App1
3	541.5	80.6	120	2 US-09-490-070A-36	Sequence 36, App1
4	541.5	80.6	120	2 US-09-490-070A-59	Sequence 59, App1
5	541.5	80.6	120	2 US-09-490-153-36	Sequence 36, App1
6	541.5	80.6	120	2 US-09-490-153-59	Sequence 59, App1
7	541.5	80.6	120	2 US-09-490-324-36	Sequence 36, App1
8	541.5	80.6	120	2 US-09-490-324-59	Sequence 59, App1
9	528	78.6	117	2 US-09-052-769B-22	Sequence 22, App1
10	528	78.6	117	2 US-09-490-070A-22	Sequence 22, App1
11	528	78.6	117	2 US-09-490-153-22	Sequence 22, App1
12	528	78.6	117	2 US-09-490-324-22	Sequence 22, App1
13	526	78.3	470	2 US-09-859-053-28	Sequence 28, App1
14	513	76.3	125	2 US-09-199-149-3	Sequence 3, App1
15	510	76.0	128	1 US-08-204-047-22	Sequence 22, App1
16	510.5	76.0	128	2 US-08-964-690-22	Sequence 22, App1
17	510	75.9	129	1 US-08-561-521-45	Sequence 45, App1
18	510	75.9	129	1 US-08-535-539A-77	Sequence 77, App1
19	510	75.9	129	4 PCT-US95-01219-45	Sequence 45, App1
20	504	75.0	123	2 US-10-330-613A-21	Sequence 21, App1
21	502	74.7	123	1 US-08-477-877B-94	Sequence 94, App1
22	502	74.7	123	1 US-08-412-281A-94	Sequence 94, App1
23	502	74.7	123	1 US-08-477-989B-94	Sequence 94, App1
24	502	74.7	123	2 US-09-452-140D-102	Sequence 102, App1
25	502	74.7	123	2 US-09-442-140D-105	Sequence 105, App1
26	501	74.6	119	1 US-08-561-521-10	Sequence 10, App1
27	501	74.6	119	4 PCT-US95-01219-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-09-025-769B-16
; Sequence 36, Application US/09025769B
; Patent No. 6300064

GENERAL INFORMATION:
 / APPLICANT: Knappik, Achim
 / APPLICANT: Pack, Peter
 / APPLICANT: Ilag, Vic
 / APPLICANT: Ge, Liming
 / APPLICANT: Moroney, Simon
 / APPLICANT: Plietzschun, Andreas
 / TITLE OF INVENTION: Protein/(Poly)peptide libraries
 / NUMBER OF SEQUENCES: 373
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: James P. Haley, Jr., Esq. c/o Fish & Neave
 / STREET: 1251 Avenue of the Americas
 / CITY: New York
 / STATE: New York
 / COUNTRY: USA
 / ZIP: 10021
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/025,769B
 / FILING DATE: 18-FEB-1998
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: EP 95 11 3021.0
 / FILING DATE: 18-AUG-1995
 / ATTORNEY/AGENT INFORMATION:
 / NAME: James P. Haley, Jr., Esq.
 / REGISTRATION NUMBER: 27,794
 / REFERENCE/DOCKET NUMBER: MORPHO/5
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (212)596-9000
 / TELEFAX: (212)596-9000
 / INFORMATION FOR SEQ ID NO: 36:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 120 amino acids
 / TYPE: amino acid
 / STRANDEDNESS:
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-09-025-769B-16

SUMMARIES

* %

Qy 1 QVQLVQSGAEVKKPGASVKKVSKCKASGYFTSYDINYVRAQTQGLEMWGMWNPNSGNTDY 60
 Db 1 QVQLVQSGAEVKKPGASVKKVSKCKASGYFTSYDINYVRAQTQGLEMWGMWNPNSGNTDY 60

RESULT 3
 US-09-490-070A-36
 ; Sequence 36, Application US/09490070A
 ; Patent No. 6996248

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Colin G. Sandcock, Esq. c/o Heller Ehrman
 STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 ZIP: 20006

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,070A
 FILING DATE: 24-Jan-2000
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandcock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 36:
 LENGTH: 120 amino acids
 TYPE: amino acid
 STRANDBNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 US-09-490-070A-36

Query Match 80.6%; Score 541.5; DB 2; Length 120;
 Best Local Similarity 84.0%; Pred. No. 1.7e-44;
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKKVSKCKASGYFTSYDINYVRAQTQGLEMWGMWNPNSGNTDY 60
 Db 1 QVQLVQSGAEVKKPGASVKKVSKCKASGYFTSYDINYVRAQTQGLEMWGMWNPNSGNTDY 60

RESULT 4
 US-09-490-070A-59
 ; Sequence 59, Application US/09490070A

Patent No. 6696248
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Colin G. Haley, Jr., Esq. c/o Fish & Neave
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,070A
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:
 US-09-490-070A-59

Query Match 80.6%; Score 541.5; DB 2; Length 120;
 Best Local Similarity 84.0%; Pred. No. 1.7e-44;
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QVQLVQSGAEVTKPGASVKVSKASCGVFTSYDINVRQATQGLEMGMWNPNSGNTDY 60
 Db 1 QVQLVQSGAEVTKPGASVKVSKASCGVFTSYDINVRQATQGLEMGMWNPNSGNTDY 60

Qy 1 QVQLVQSGAEVTKPGASVKVSKASCGVFTSYDINVRQATQGLEMGMWNPNSGNTDY 60
 Db 1 QVQLVQSGAEVTKPGASVKVSKASCGVFTSYDINVRQATQGLEMGMWNPNSGNTDY 60

Qy 61 AOKPQGRVTTMRTDTSISTAYMELSSLSASDATTAYCVRGFGVSYNDYYKGMDWVNGQTT 120
 Db 61 AOKPQGRVTTMRTDTSISTAYMELSSLSASDATTAYCVRGFGVSYNDYYKGMDWVNGQTT 115

Qy 121 VTVSS 125
 Db 116 VTVSS 120

RESULT 6
 US-09-490-153-59
 Sequence 59, Application US/09490153
 Patent No. 6706484
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 STREET: 1251 Avenue of the Americas
 CITY: New York

RESLT 5
 US-09-490-153-36
 Sequence 36, Application US/09490153
 Patent No. 6706484
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas

```

STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esg.
REGISTRATION NUMBER: 27 794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-153-59

Query Match Score 541.5; DB 2; Length 120;
Best Local Similarity 84.0%; Pred. No. 1.7e-44; Mismatches 10; Indels 5
Matches 105; Conservative 5; Mismatches 10; Indels 5

Qy 1 QVOLYQSAEVKPGASVKSCASGTYFTSYIDINWROTGGQGLEMMGMINW
Db 1 QVQLQSAEVKPGASVKSCASGTYFTSYIDINWROTGGQGLEMMGMINW
Qy 61 AQQFQGRVMTTRDTISITAYMELSSIRSEDTAIIYCYRGFGYSSNYDYYGMM
Db 61 AQQFQGRVMTTRDTISITAYMELSSIRSEDTAIIYCYRGFGYSSNYDYYGMM
Qy 121 VTVSS 125
Db 116 VTVSS 120

RESULT 7
US-09-490-324-36
; Sequence 36, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly) peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esg., c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490, 324
 FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025, 769
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORBHO/5

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 US-09-490-324-36

	Query Match	Score	DB 2;	Length
Qy	1 QVQLVQSGAERVKPGASVKSAGSAGYPTSYIDINVRQATGQGLEMWGWINI 1 QVQLVQSGAERVKPGASVKSAGSAGYPTSYIDINVRQATGQGLEMWGWINI	80.6%; Best Local Similarity Matches 105;	541.5%; Pred. No. 1.7e-44; Conservative 5; Mismatches 10;	120;
Db	61 AQQFQGRVITMTRDTISIATAYMELSSLRSEDTAYCVRGFGYSYNDYYGMI 61 AQQFQGRVITMTRDTISIATAYMELSSLRSEDTAYCVRGFGYSYNDYYGMI	80.6%; Best Local Similarity Matches 105;	541.5%; Pred. No. 1.7e-44; Conservative 5; Mismatches 10;	120;
Qy	121 VTVSS 125 116 VTVSS 120			
Db				

RESULT 8
 US-09-490-324-59
 ; Sequence 59, Application US/09/490324
 ; Patent No. 6828122

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Illeg, Vic
 Ge, Liming
 Moroney, Simon
 Pieleckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490, 324
 FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025, 769

FILED DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEFAX: (212) 596-9000
 INFORMATION FOR SBO ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:
 US-09-490-324-59

Query Match 80.6%; Score 541.5; DB 2; Length 120;
 Best Local Similarity 84.0%; Pred. No. 1.7e-44;
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QVOLVQSGAEVKPGASVKSCKASGYTFTSDINWYRQATCGLEMMGWNPNSGNTDY 60
 Db 1 QVOLVQSGAEVKPGASVKSCKASGYTFTSDINWYRQATCGLEMMGWNPNSGNTNY 60

Qy 61 AOKPQRVUTMRTDTISIAYMELSSLASEDTAIIYCYRGFYSYNTDYYGMDVWGCGTT 120
 Db 61 AOKPQRVUTMRTDTISIAYMELSSLASEDTAIIYCYRGFYSYNTDYYGMDVWGCGTT 115

RESULT 10
 1 Sequence 22, Application US/09490070A
 Patent No. 669648

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries
 NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-09-025-769B-22

Query Match 78.6%; Score 528; DB 2; Length 117;
 Best Local Similarity 82.5%; Pred. No. 3.2e-43;
 Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

Qy 1 QVOLVQSGAEVKPGASVKSCKASGYTFTSDINWYRQATCGLEMMGWNPNSGNTDY 60
 Db 1 QVOLVQSGAEVKPGASVKSCKASGYTFTSDINWYRQATCGLEMMGWNPNSGNTNY 60

Qy 61 AQRFGRTUTMRTDTISIAYMELSSLASEDTAIIYCYRGFYSYNTDYYGMDVWGCGTT 119
 Db 61 AQRFGRTUTMRTDTISIAYMELSSLASEDTAIIYCYRGFYSYNTDYYGMDVWGCGTT 111

RESULT 125
 1 Sequence 22, Application US/09490070A
 Patent No. 669648

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly) peptide libraries
 NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,070A
 FILING DATE: 24-JUN-2000

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLogy: linear
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 22:
us-09-490-070A-22

Query Match 78.6%; Score 528; DB 2; Length 117;
Best Local Similarity 82.5%; Pred. No. 3.2e-43;
Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

1 QVQLVQSGAETYKPGASVKVSCKASGFTSYDINVRQATCQGLEMWGWINPNSGNTY 60
Db 1 QVQLVQSGAETYKPGASVKVSCKASGFTSYDINVRQATCQGLEMWGWINPNSGNTY 60

1 AQKFGQRTMTRDTSISIAYMELSSRLRSDDTAYTCVRFQGYSYNYDYYGMDWGQGT 11
Db 1 AQKFGQRTMTRDTSISIAYMELSSRLRSDDTAYTCVRFQGYSYNYDYYGMDWGQGT 11

1 QVQLVQSGAETYKPGASVKVSCKASGFTSYDINVRQATCQGLEMWGWINPNSGNTY 60
Db 1 QVQLVQSGAETYKPGASVKVSCKASGFTSYDINVRQATCQGLEMWGWINPNSGNTY 60

61 AQKFGQRTMTRDTSISIAYMELSSRLRSDDTAVYTCARDGDD-----GFDYNGQGT 111
Db 61 AQKFGQRTMTRDTSISIAYMELSSRLRSDDTAVYTCARDGDD-----GFDYNGQGT 111

RESULT 12
US-09-490-324-22
; Sequence 22, Application US/09490324
; Patent No. 6828422

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
; Plueckthun, Andreas
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
PATENT IN RELEASE NUMBER: EP 95 11 3021.0
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 22:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
LENGTH: 117 amino acids
STRANDEDNESS: <Unknown>
TOPOLOGY: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
Query Match 78.6%; Score 528; DB 2; Length 117;
Best Local Similarity 82.5%; Pred. No. 3.2e-43;
Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

1 QVQLVQSGAETYKPGASVKVSCKASGFTSYDINVRQATCQGLEMWGWINPNSGNTY 60
Db 1 QVQLVQSGAETYKPGASVKVSCKASGFTSYDINVRQATCQGLEMWGWINPNSGNTY 60

1 AQKFGQRTMTRDTSISIAYMELSSRLRSDDTAYTCVRFQGYSYNYDYYGMDWGQGT 11
Db 1 AQKFGQRTMTRDTSISIAYMELSSRLRSDDTAYTCVRFQGYSYNYDYYGMDWGQGT 11

Db 61 AQRFGRTVMTRTSISAYMELSSRLSDTAVYCARDGDG-----GFDYMGQT 111
 Qy 120 VTVYSS 125
 Db 112 LTVYSS 117

RESULT 1.3
 US-09-859-053-28
 ; Sequence 28, Application US/09859053
 ; Patent No. 6803039
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsuji, Takashi
 ; APPLICANT: Teruka, Katsunari
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND PHARMACEUTICAL USE THEREOF
 ; FILE REFERENCE: 06/301-079001
 ; CURRENT APPLICATION NUMBER: US/09/859,053
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: JP 2001-99508
 ; PRIOR FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: JP 2000-147116
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 28
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-859-053-28

Query Match 78.3% Score 526; DB 2; Length 470;
 Best Local Similarity 79.2% Prod. No. 2.e-4;
 Matches 99; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 QVQLVQSAEVKPGASVKVSKASGTTFTSDINWVQATQGLEMWGWINPNSGNTDY 60
 Db 20 QVQLVQSAEVKPGASVKVSKASGTTFTGTYMMWVQAPQGLEMWGWINPHSGCTT 79
 Qy 61 AQRFGRTVMTRTSISAYMELSSRLSDTAVYCARDGDG-----GFDYMGQT 120
 Db 80 AQRFGRTVMTRTSISAYMELSSRLSDTAVYCARDGDG-----GFDYMGQT 139

Qy 121 VTVYSS 125
 Db 140 VTVYSS 144

RESULT 14
 US-09-199-149-3
 ; Sequence 3, Application US/09199149
 ; GENERAL INFORMATION:
 ; APPLICANT: Jonak, Zdenka L.
 ; APPLICANT: Trulli, Alexander H.
 ; APPLICANT: Trulli, Jr., Stephen H.
 ; APPLICANT: Johansson, Kyung O.
 ; TITLE OF INVENTION: Humanized Monoclonal Antibodies
 ; FILE REFERENCE: P50860
 ; CURRENT APPLICATION NUMBER: US/09/199,149
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 3
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: Kabat VH subgroup I
 ; US-09-199-149-3

Query Match 76.3% Score 513; DB 2; Length 125;

Db 1 QVQLVQSAEVKPGASVKVSKASGTTFTSDINWVQATQGLEMWGWINPNSGNTDY 59
 1 QVQLVQSAEVKPGASVKVSKASGTTFTGTYMMWVQAPQGLEMWGWINPHSGCTT 60

Best Local Similarity 80.6% Prod. No. 9.3e-42;
 Matches 104; Conservative 8; Mismatches 9; Indels 8; Gaps 5;

Qy 1 QVQLVQSAEVKPGASVKVSKASGTTFTSDINWVQATQGLEMWGWINPNSGNTDY 60
 Db 1 QVQLVQSAEVKPGASVKVSKASGTTFTGTYMMWVQAPQGLEMWGWINPHSGCTT 59

Qy 61 AQRFGRTVMTRTSISAYMELSSRLSDTAVYCARDGDG-----GFDYMGQT 116
 Db 60 AQRFGRTVMTRTSISAYMELSSRLSDTAVYCARPQTYGGCCYGY-WYWG--WVG 116
 Qy 117 QTVTVSS 125
 Db 117 QTVTVSS 125

RESULT 15
 US-08-202-047-22
 ; Sequence 22, Application US/08202047
 ; Patent No. 5800815
 ; GENERAL INFORMATION:
 ; APPLICANT: CHERNUT, Robert W.
 ; APPLICANT: POLLIE, Margaret J.
 ; APPLICANT: PAULSON, James C.
 ; APPLICANT: JONES, S. Tarran
 ; APPLICANT: SALDANHA, Jose W.
 ; APPLICANT: BENDIG, Mary M.
 ; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Stewart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/202,047
 ; FILING DATE: 25-FEB-1994
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 14137-77
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2420
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 128 amino acids
 ; TYPE: amino acid
 ; STRANDBEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1-128
 ; OTHER INFORMATION: /label= HUMAN_I
 ; US-08-202-047-22

Query Match 76.0% Score 510.5; DB 1; Length 128;
 Best Local Similarity 77.9% Prod. No. 1.e-41;
 Matches 102; Conservative 7; Mismatches 13; Indels 9; Gaps 3;

Qy 1 QVQLVQSAEVKPGASVKVSKASGTTFTSDINWVQATQGLEMWGWINPNSGNTDY 59
 1 QVQLVQSAEVKPGASVKVSKASGTTFTGTYMMWVQAPQGLEMWGWINPHSGCTT 60

Qy 60 YAQKFQGRVMTRDTSISAYMELSSLRSEDAIYCVRGFGS---YNYDYYGMDV 114
Db 61 YAQKFQERVITADTSISAYMELSSLRSEDAVYCARAPGYGSGGCTRGDFP---DY 117
Qy 115 WCGGTTVYSS 125
Db 118 WCGGTLVYSS 128

Search completed: May 15, 2006, 17:06:02
Job time : 36.4077 sec_B

Result No.	Score	Query	Match	Length	DB	ID	Description
1	672	100.0	125	4	US-10-041-860-48		Sequence 48, App
2	672	100.0	125	4	US-10-041-860-200		Sequence 200, App
3	672	100.0	125	4	US-10-041-860-237		Sequence 237, App
4	672	100.0	125	4	US-10-041-860-372		Sequence 372, App
5	672	100.0	125	4	US-10-041-860-383-2		Sequence 2, App
6	638	94.9	125	4	US-10-041-860-38		Sequence 38, App
7	638	94.9	125	4	US-10-041-860-203		Sequence 203, App
8	638	94.9	125	4	US-10-041-860-240		Sequence 240, App
9	638	94.9	125	4	US-10-041-860-343		Sequence 343, App
10	638	94.9	125	4	US-10-041-860-385-54		Sequence 54, App
11	593.5	88.3	126	4	US-10-041-860-19		Sequence 19, App
12	593.5	88.3	126	4	US-10-041-860-201		Sequence 201, App
13	593.5	88.3	126	4	US-10-041-860-288		Sequence 288, App
14	593.5	88.3	126	4	US-10-041-860-38-18		Sequence 18, App
15	579.5	86.2	125	4	US-10-041-860-238		Sequence 238, App
16	575.5	85.6	126	4	US-10-041-860-40		Sequence 40, App
17	575.5	85.6	126	4	US-10-041-860-204		Sequence 204, App
18	575.5	85.6	126	4	US-10-041-860-241		Sequence 241, App
19	575.5	85.6	126	4	US-10-041-860-349		Sequence 349, App
20	575.5	85.6	126	4	US-10-041-860-58		Sequence 58, App
21	572	85.1	127	4	US-10-041-860-44		Sequence 44, App
22	572	85.1	127	4	US-10-041-860-205		Sequence 205, App
23	572	85.1	127	4	US-10-041-860-242		Sequence 242, App
24	572	85.1	127	4	US-10-041-860-360		Sequence 360, App
25	572	85.1	127	4	US-10-041-860-33-66		Sequence 66, App
26	567.5	84.4	126	4	US-10-041-860-21		Sequence 21, App
27	567.5	84.4	126	4	US-10-041-860-199		Sequence 199, App

APPLICANT: Feng, Xiao
 APPLICANT: Yang, Xiao-Dong
 APPLICANT: Chen, Francine
 APPLICANT: Gazit, Gadi
 APPLICANT: Weber, Richard
 APPLICANT: Bezbabet, Binyam
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: AGENIX.051A
 CURRENT APPLICATION NUMBER: US/10/041,860
 CURRENT FILING DATE: 2002-01-07
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 200
 LENGTH: 125
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-200

Query Match 100.0%; Score 672; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 8.6e-54;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTD 60
 Db 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTD 60

Qy 61 AQQFQGRVTMTRDTISIATAMELSSRSQEDTAIYCYVRGFGSYNTYYGMDVWQGTT 120
 Db 61 AQQFQGRVTMTRDTISIATAMELSSRSQEDTAIYCYVRGFGSYNTYYGMDVWQGTT 120

Qy 121 VTVSS 125
 Db 121 VTVSS 125

RESULT 4
 US-10-041-860-372
 Sequence 3/2, Application US/10041860
 Publication No. US20030157109A1
 GENERAL INFORMATION:
 APPLICANT: Corvalan, Jose R.P.
 APPLICANT: Jia, Xiao-Chi
 APPLICANT: Feng, Xiao
 APPLICANT: Yang, Xiao-Dong
 APPLICANT: Chen, Francine
 APPLICANT: Gazit, Gadi
 APPLICANT: Weber, Richard
 APPLICANT: Bezbabet, Binyam
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: AGENIX.051A
 CURRENT APPLICATION NUMBER: US/10/041,860
 CURRENT FILING DATE: 2002-01-07
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 372
 LENGTH: 125
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-372

Query Match 100.0%; Score 672; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 8.6e-54;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTD 60
 Db 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTD 60

Qy 61 AQQFQGRVTMTRDTISIATAMELSSRSQEDTAIYCYVRGFGSYNTYYGMDVWQGTT 120
 Db 61 AQQFQGRVTMTRDTISIATAMELSSRSQEDTAIYCYVRGFGSYNTYYGMDVWQGTT 120

Qy 121 VTVSS 125
 Db 121 VTVSS 125

RESULT 5
 US-10-665-383-2
 Sequence 2, Application US/10665383
 Publication No. US20040141969A1
 GENERAL INFORMATION:
 APPLICANT: Ploeg, Juergen
 APPLICANT: Gazit, Gadi
 APPLICANT: Keyt, Bruce
 APPLICANT: LaRochelle, William
 APPLICANT: Lichtenstein, Henri
 TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
 TITLE OF INVENTION: USING ANTI-PDGF DD ANTIBODIES
 FILE REFERENCE: AGENIX.052A
 CURRENT APPLICATION NUMBER: US/10/665,383
 CURRENT FILING DATE: 2003-09-16
 PRIOR APPLICATION NUMBER: 60/411,137
 PRIOR FILING DATE: 2002-09-16
 NUMBER OF SEQ ID NOS: 97
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 125
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-665-383-2

Query Match 100.0%; Score 672; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 8.6e-54;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTD 60
 Db 1 QVQLVQGAEVKPGASVKVSKASGFTSYDINVRQATQGLEWMGWMNPNSGNTD 60

Qy 61 AQQFQGRVTMTRDTISIATAMELSSRSQEDTAIYCYVRGFGSYNTYYGMDVWQGTT 120
 Db 61 AQQFQGRVTMTRDTISIATAMELSSRSQEDTAIYCYVRGFGSYNTYYGMDVWQGTT 120

Query Match 100.0%; Score 672; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 8.6e-54;
 Matches 125; Conservative 0; Mismatches 0; Gaps 0;
 FILE REFERENCE: ABGENIX 051A
 TITLE OF INVENTION: THEREOF
 CURRENT APPLICATION NUMBER: US/10/041,860
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 203
 LENGTH: 125
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-203

Query Match 94.9%; Score 638; DB 4; Length 125;
 Best Local Similarity 94.4%; Pred. No. 1.1e-50;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 FILE REFERENCE: ABGENIX 051A
 TITLE OF INVENTION: THEREOF
 CURRENT APPLICATION NUMBER: US/10/041,860
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 203
 LENGTH: 125
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-203

Query Match 94.9%; Score 638; DB 4; Length 125;
 Best Local Similarity 94.4%; Pred. No. 1.1e-50;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 FILE REFERENCE: ABGENIX 051A
 TITLE OF INVENTION: THEREOF
 CURRENT APPLICATION NUMBER: US/10/041,860
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 203
 LENGTH: 125
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-203

RESULT 6
 US-10-041-860-38
 ; Sequence 38, Application US/10041860
 ; GENERAL INFORMATION:
 ; APPLICANT: corvalan, Jose R. P.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Peng, Xiao-Dong
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; TITLE OF INVENTION: ANTIODILES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX. 051A
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-38

Query Match 94.9%; Score 638; DB 4; Length 125;
 Best Local Similarity 94.4%; Pred. No. 1.1e-50;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 FILE REFERENCE: ABGENIX 051A
 TITLE OF INVENTION: THEREOF
 CURRENT APPLICATION NUMBER: US/10/041,860
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 240
 LENGTH: 125
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-240

Query Match 94.9%; Score 638; DB 4; Length 125;
 Best Local Similarity 94.4%; Pred. No. 1.1e-50;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 FILE REFERENCE: ABGENIX 051A
 TITLE OF INVENTION: THEREOF
 CURRENT APPLICATION NUMBER: US/10/041,860
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 240
 LENGTH: 125
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-240

RESULT 7
 US-10-041-860-203
 ; Sequence 203, Application US/10041860
 ; GENERAL INFORMATION:
 ; APPLICANT: corvalan, Jose R. P.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Peng, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard

RESULT 9
 US-10-041-860-143
 ; Sequence 343, Application US/10041860
 ; PUBLICAL INFORMATION: US2003157109A1
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Peng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: AGENIX 051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 343
 LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-143

Query Match 94.9%; Score 638; DB 4; Length 125;
 Best Local Similarity 94.4%; Pred. No. 1.1e-50;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKSCKASGTYFTSYDINVRQATCGLEWMGNPNSGNTGY 60
 Db 1 QVQLVQSGAEVKPGASVKSCKASGTYFTSYDINVRQATCGLEWMGNPNSGNTGY 60

Qy 61 AOKFQGRVMTRDTISIATAYMELSSRLSDETAVYCARSGSYGDDYYGMDVNGQTT 120
 Db 61 AOKFQGRVMTRNTISIATAYMELSSRLSDETAVYCARSGSYGDDYYGMDVNGQTT 120

Qy 121 VTVSS 125
 Db 121 VTVSS 125

RESULT 10
 US-10-665-383-54
 ; Sequence 54, Application US/10665383
 ; PUBLICAL INFORMATION: US/10/665,383
 ; CURRENT APPLICATION NUMBER: US/10/665,383
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: 60/411,137
 ; NUMBER OF SEQ ID NOS: 97
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 54
 LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-665-383-54

Query Match 94.9%; Score 638; DB 4; Length 125;
 Best Local Similarity 94.4%; Pred. No. 1.1e-50;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 11
 US-10-041-860-19
 ; Sequence 19, Application US/10041860
 ; PUBLICAL INFORMATION: US2003157109A1
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Peng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: AGENIX 051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 19
 LENGTH: 126
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-19

Query Match 88.3%; Score 593.5; DB 4; Length 126;
 Best Local Similarity 89.7%; Pred. No. 1.3e-6;
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKPGASVKSCKASGTYFTSYDINVRQATCGLEWMGNPNSGNTGY 60
 Db 1 QVQLVQSGAEVKPGASVKSCKASGTYFTSYDINVRQATCGLEWMGNPNSGNTGY 60

Qy 61 AOKFQGRVMTRDTISIATAYMELSSRLSDETAVYCARSGSYGDDYYGMDVNGQTT 119
 Db 61 AOKFQGRVMTRNTISIATAYMELSSRLSDETAVYCARSGSYGDDYYGMDVNGQTT 120

Qy 120 VTVSS 125
 Db 121 VTVSS 126

RESULT 12
 US-10-041-860-201
 ; Sequence 201, Application US/10041860
 ; PUBLICAL INFORMATION: US2003157109A1
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Peng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: AGENIX 051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860

Query Match 94.9%; Score 638; DB 4; Length 125;
 Best Local Similarity 94.4%; Pred. No. 1.1e-50;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Flegge, Juergen
; APPLICANT: Gazi, Gadi
; APPLICANT: Keye, Bruce
; APPLICANT: Lakocheine, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; CURRENT APPLICATION NUMBER: US-10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIORITY APPLICATION NUMBER: 60/411,137
; PRIORITY FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match 88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
Qy 1 QVQLVQSGAEVKPGASVKCSKASGTTFTSDINWROATCGLEMGWNPNSGNTDY 60
Db 1 QVQLVQSGAEVKPGASVKCSKASGTTFTSDINWROATCGLEMGWNPNSGNTGY 60
Qy 61 AQQFQGRVMTMRTTSIATAYMELSSRLSRTDAIYCYCVR-GFGSYNTDYYGMDVNGQGT 119
Db 61 AQQFQGRVMTMRTTSIATAYMELSSRLSRTDAIYCYCVR-GFGSYNTDYYGMDVNGQGT 120
Qy 120 TVTVSS 125
Db 121 TVTVSS 126

RESULT 13
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazi, Gadi
; APPLICANT: Weber, Richard
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX 051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288

Query Match 88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
Qy 1 QVQLVQSGAEVKPGASVKCSKASGTTFTSDINWROATCGLEMGWNPNSGNTDY 60
Db 1 QVQLVQSGAEVKPGASVKCSKASGTTFTSDINWROATCGLEMGWNPNSGNTGY 60
Qy 61 AQQFQGRVMTMRTTSIATAYMELSSRLSRTDAIYCYCVR-GFGSYNTDYYGMDVNGQGT 119
Db 61 AQQFQGRVMTMRTTSIATAYMELSSRLSRTDAIYCYCVR-GFGSYNTDYYGMDVNGQGT 120
Qy 120 TVTVSS 125
Db 121 TVTVSS 126

RESULT 15
US-10-041-860-238
; Sequence 238, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazi, Gadi
; APPLICANT: Weber, Richard
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX 051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-238

Query Match 88.2%; Score 579.5; DB 4; Length 125;
Best Local Similarity 89.4%; Pred. No. 2.5e-45;
Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
Qy 4 LVQSGAEVKPGASVKCSKASGTTFTSDINWROATCGLEMGWNPNSGNTDYAQK 63
Db 3 LVQSGAEVKPGASVKCSKASGTTFTSDINWROATCGLEMGWNPNSGNTGYAQK 62
Qy 5 LVQSGAEVKPGASVKCSKASGTTFTSDINWROATCGLEMGWNPNSGNTGYAQK 64
Db 3 LVQSGAEVKPGASVKCSKASGTTFTSDINWROATCGLEMGWNPNSGNTGYAQK 62

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Db 63 FQGRVMTRTSISTAYMELSSLRSEDTAVYCCAREGIAVAGTYYYGMDWGQGTTVT 122
Qy 123 VSS 125
Db 123 VSS 125

Search completed: May 15, 2006, 17:25:06
Job time : 127.073 secs

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OM protein - protein search, using sw model

Run on: May 15, 2006, 17:21:22 ; Search time 19.8498 Seconds (without alignments)

295.651 Million cell updates/sec

Title: US-10-041-860-48

Perfect score: 672

Sequence: 1 QVQIVQSGAEVKPGASVKKV. YDYYGMDVWGQCTTVTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:*

1: /SIDSS5/ptodata/1/pubpa/US08_NEW_PUB.PEP1:*

2: /SIDSS5/ptodata/1/pubpa/US06_NEW_PUB.PEP1:*

3: /SIDSS5/ptodata/1/pubpa/US07_NEW_PUB.PEP1:*

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9: /SIDSS5/ptodata/1/pubpa/US10_NEW_PUB.PEP1:*

10: /SIDSS5/ptodata/1/pubpa/US11_NEW_PUB.PEP1:*

11: /SIDSS5/ptodata/1/pubpa/US11_NEW_PUB.PEP1:*

12: /SIDSS5/ptodata/1/pubpa/US60_NEW_PUB.PEP1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	%
1	561.5	83.6	122	9	US-10-082-440-61	Sequence 61, App1	
2	558.5	83.1	145	9	US-10-721-763-29	Sequence 29, App1	
3	541.5	81.3	124	11	US-11-040-159-8	Sequence 8, App1	
4	541.5	80.6	120	9	US-10-834-397-36	Sequence 36, App1	
5	541.5	80.6	120	9	US-10-834-397-59	Sequence 59, App1	
6	536.5	79.8	247	11	US-11-514-515-1729	Sequence 1729, App1	
7	536.5	79.8	247	11	US-11-266-444-1729	Sequence 1729, App1	
8	536	79.8	125	9	US-10-982-440-45	Sequence 45, App1	
9	534.5	79.5	249	11	US-11-054-515-919	Sequence 919, App1	
10	534.5	79.5	249	11	US-11-266-444-919	Sequence 919, App1	
11	528	78.6	117	9	US-10-834-397-22	Sequence 22, App1	
12	527.5	78.5	122	10	US-11-211-917-110	Sequence 110, App1	
13	524.5	78.1	245	11	US-11-054-515-1896	Sequence 1896, App1	
14	524.5	78.1	245	11	US-11-266-444-1816	Sequence 1896, App1	
15	524	78.0	255	11	US-11-054-515-1407	Sequence 1407, App1	
16	524	78.0	255	11	US-11-266-444-1407	Sequence 1407, App1	
17	523.5	77.9	247	11	US-11-054-515-927	Sequence 927, App1	
18	523.5	77.9	247	11	US-11-054-515-948	Sequence 948, App1	
19	523.5	77.9	247	11	US-11-266-444-927	Sequence 927, App1	
20	523.5	77.9	247	11	US-11-266-444-948	Sequence 948, App1	
21	520	77.4	256	11	US-11-054-515-1301	Sequence 1301, App1	

RESULT 1
US-10-982-440-61
/ Sequence 61, Application US/10982440
/ Publication No. US20060018909A1
/ GENERAL INFORMATION:
/ APPLICANT: Oliner, John
/ INVENTION: Argiropoietin-2 Specific Binding Agents
/ TITLE OF INVENTION: Argiropoietin-2 Specific Binding Agents
/ FILE REFERENCE: 04-881-A
/ CURRENT APPLICATION NUMBER: US/10/982,440
/ PRIOR FILING DATE: 2004-11-04
/ PRIOR APPLICATION NUMBER: 60/620,161
/ PRIOR FILING DATE: 2004-10-19
/ NUMBER OF SEQ ID NOS: 215
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 61
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-982-440-61

Query Match 83.6%; Score 561.5; DB 9; Length 122;
Best Local Similarity 86.4%; Pred. No. 2.3e-44; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVQLVSGAELYKKPGASVKKVSKASGYTFTSYDINVRQATGQGLEWMGTPNPGSGNTDY 60
Db 1 QVQLVSGAELYKKPGASVKKVSKASGYTFTSYDINVRQATGQGLEWMGTPNPGSGNTGY 60

Qy 61 AQKPGQGRVMTRDTSTISATMELSSLRSEDATIAYVYCVRGFQSYSYNYYGMDVNGQGTT 120
Db 61 AQKPGQGRVMTRDTSTISATMELSSLRSEDATIAYVYCAKEIAVA--GTRYGMDVNGQGTT 117

RESULT 2
US-10-721-763-29
/ Sequence 29, Application US/10721763
/ Publication No. US2005249729A1
/ GENERAL INFORMATION:
/ APPLICANT: KIRIN BEER KABUSHIKI KAISHA

TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
 FILE REFERENCE: PH-1573-PCT
 CURRENT APPLICATION NUMBER: US/10/721,763
 CURRENT FILING DATE: 2003-11-26
 PRIORITY APPLICATION NUMBER: JP2001-150213
 PRIOR FILING DATE: 2001-05-11
 PRIORITY APPLICATION NUMBER: JP2001-243040
 PRIOR FILING DATE: 2001-08-09
 PRIORITY APPLICATION NUMBER: JP2001-314489
 PRIOR FILING DATE: 2001-10-11
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 29
 LENGTH: 145
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-721-763-29

Query Match 83.1%; Score 558.5%; DB 9; Length 145;
 Best Local Similarity 83.3%; Pred. No. 5.1e-44;
 Matches 105; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKPGASVKVSKASGYTFSYDINWROATGQLEWNGWINPNSGNTDY 60
 Db 20 QVQLVQSGAEVKPGASVKVSKASGYTFSYDINWROATGQLEWNGWINPNSGNTDY 60

Qy 61 AQKFGQRTMTRDTISIATAYMELSSRSEDTAYCVRGCGY-STQNYDTYGMDWGQTT 119
 Db 80 PQKFGQRTMTRDTISIATAYMELSSRSEDTAYCVRGCGY-STQNYDTYGMDWGQTT 139

Qy 120 TVTVSS 125
 Db 140 TVTVSS 145

RESULT 4
 US-10-834-397-36
 Sequence 36, Application US/10834397
 Publication No. US2006000334A1
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Illeg, Vic
 Ge, Liming
 Moroney, Simon
 Blueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CURRENT APPLICATION ADDRESS:
 CORRESPONDENCE ADDRESS:
 ADDRESSER: James P. Haley, Jr., Eqq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 ZIP: 10021
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/834,397
 FILING DATE: 29-Apr-2004
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,324
 FILING DATE: 24-Jan-2000
 APPLICATION NUMBER: US/09/025,769
 FILING DATE: 16-FEB-1998
 APPLICATION NUMBER: BP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James P. Haley, Jr., Eqq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 36:
 LENGTH: 120 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 US-10-834-397-36

OTHER INFORMATION: Description of Artificial Sequence:BA130-5-E10 Vh human
 OTHER INFORMATION: variable region containing minimal essential binding
 OTHER INFORMATION: specificity domain (MBSD) in heavy chain CDR3 from murine
 OTHER INFORMATION: anti-PcrV antibody M166 and complete human J-region (JH6)
 US-11-040-159-8

Query Match 81.3%; Score 546.5%; DB 11; Length 124;
 Best Local Similarity 83.2%; Pred. No. 5.4e-43;
 Matches 104; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKPGASVKVSKASGYTFSYDINWROATGQLEWNGWINPNSGNTDY 60
 Db 1 QVQLVQSGAEVKPGASVKVSKASGYTFSYDINWROATGQLEWNGWINPNSGNTDY 60

Qy 61 AOKFOGRITMTRDTISIATAYMELSSLRSEDATAYYCVRGFGSYNDDYKGMDDVNGQTT 120
 Db 61 AOKFOGRITMTRDTISIATAYMELSSLRSEDATAYYCARWGG----DGFYAMDYNGQTT 115

Qy 121 VTVSS 125
 Db 116 VTVSS 120

RESULT 5
 US-10-834-397-59
 Sequence 59, Application US/10834397
 Publication No. US2006000333411
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Pueckthun, Andreas
 TITLE OF INVENTION: Protein (Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORMATE
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/834,397
 FILING DATE: 29-Apr-2004
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,324
 FILING DATE: 24-Jan-2000
 APPLICATION NUMBER: US/09/025,769
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:
 us-10-834-397-59

Query Match 80.6%; Score 541.5; DB 9; Length 120;
 Best Local Similarity 84.0%; Pred. No. 1.5e-42;
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 OYLVQSGAEVKPGASVKVSKCAKGTYTSDINWYRQATQGLEWMGWINPNSGNTDY 60
 Db 1 OYLVQSGAEVKPGASVKVSKCAKGTYTSDINWYRQATQGLEWMGWINPNSGNTY 60

Qy 61 AOKFOGRITMTRDTISIATAYMELSSLRSEDATAYYCVRGFGSYNDDYKGMDDVNGQTT 120
 Db 61 AOKFOGRITMTRDTISIATAYMELSSLRSEDATAYYCARWGG----DGFYAMDYNGQTT 115

Qy 121 VTVSS 125
 Db 116 VTVSS 120

RESULT 6
 US-11-054-515-1729
 Sequence 1729, Application US/11054515
 Publication No. US005025532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PFS23P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,297
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO: 1729
 LENGTH: 247
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-1729

Query Match 79.8%; Score 536.5; DB 11; Length 247;
 Best Local Similarity 81.6%; Pred. No. 8.7e-42;
 Matches 102; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 OYLVQSGAEVKPGASVKVSKCAKGTYTSDINWYRQATQGLEWMGWINPNSGNTDY 60
 Db 1 OYLVQSGAEVKPGASVKVSKCAKGTYTSDINWYRQATQGLEWMGWINPNSGNTY 60

Qy 61 AOKFOGRITMTRDTISIATAYMELSSLRSEDATAYYCVRGFGSYNDDYKGMDDVNGQTT 120
 Db 61 AOKFOGRITMTRDTISIATAYMELSSLRSEDATAYYCARWGG----DGFYAMDYNGQTT 119

Qy 121 VTVSS 125
 Db 120 VTVSS 124

RESULT 7
 US-11-266-444-1729
 Sequence 1729, Application US/11266444
 Publication No. US20060062789A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
 FILE REFERENCE: PFS23P1D1
 CURRENT APPLICATION NUMBER: US/11/266,444
 PRIOR FILING DATE: 2005-11-04
 PRIOR APPLICATION NUMBER: 09/880,746
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/212,210
 PRIOR FILING DATE: 2000-06-16

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PRIORITY APPLICATION NUMBER: 60/240,816
; PRIORITY FILING DATE: 2000-10-17
; PRIORITY APPLICATION NUMBER: 60/276,248
; PRIORITY FILING DATE: 2001-03-16
; PRIORITY APPLICATION NUMBER: 60/277,379
; PRIORITY FILING DATE: 2001-03-21
; PRIORITY APPLICATION NUMBER: 60/293,499
; PRIORITY FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1729
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1729

Query Match 79.8%; Score 536.5; DB 11; Length 247;
Best Local Similarity 81.6%; Pred. No. 8.7e-42; Indels 1; Gaps 1;
Matches 102; Conservative 8; Mismatches 14; Del 1; Gap 1;

Qy 1 QVQLVSGAELYKPGASVKYSCKASGYTFSYDINVRQATGQGLEWMGWINPNSGGNTDY 60
Db 1 QVQLVSGAELYKPGASVKYSCKASGYTFSYDINVRQATGQGLEWMGWINPNSGGNTNY 60

Qy 61 AQKFGQRVMTRDTSTIATYMEISSLRSDETAIYCVRGFGYSTNYDYYGMDVWGQGTT 120
Db 61 AQKFGQRVMTRDTSTIATYMEISSLRSDETAIYCVRGFGYSTNYDYYGMDVWGQGTT 120

Qy 121 VTVSS 125
Db 120 VTVSS 124

RESULT 8
US-10-982-440-45
Sequence 45, Application US/10992440
; Publication No. US2006018909A1
GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agent 6
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-45

Query Match 79.8%; Score 536.5; DB 9; Length 125;
Best Local Similarity 81.6%; Pred. No. 4.9e-42; Indels 0; Gaps 0;
Matches 102; Conservative 7; Mismatches 16; Del 1; Gap 1;

Qy 1 QVQLVSGAELYKPGASVKYSCKASGYTFSYDINVRQATGQGLEWMGWINPNSGGNTDY 60
Db 1 QVQLVSGAELYKPGASVKYSCKASGYTFSYDINVRQATGQGLEWMGWINPNSGGNTNY 60

Qy 61 AQKFGQRVMTRDTSTIATYMEISSLRSDETAIYCVRGFGYSTNYDYYGMDVWGQGTT 120
Db 61 AQKFGQRVMTRDTSTIATYMEISSLRSDETAIYCVRGFGYSTNYDYYGMDVWGQGTT 120

Qy 121 VTVSS 125
Db 121 VTVSS 125

RESULT 9
US-11-054-515-919

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; Sequence 919, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PP523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-04-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PAA
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 919
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-919

Query Match 79 5% ; Score 534.5; DB 11; Length 249;
Best Local Similarity 81.7%; Pred. No. 1.3e-41;
Matches 103; Conservative 8; Mismatches 14; Indels 1;

Db 1 QVQLVQSGAEVKPKPAGSVKVSCKASQSYTFTSYDINWVRQATGQGLWMGWINPNA
Qy 61 AQQPQGRVMTTRDTSTAYMELSLRSRSEDTAIVYCVRGFGRSYNTYY-YGMD
Db 61 AQQPQGRVMTTRNTSISTAYMELSLRSRSEDTAVYIARGTYDILTGFYHGMQ
Qy 120 TVTVSS 125
Db 121 TVTVSS 126

RESULT 10
US-11-266-444-919
; Sequence 919, Application US/11266444
; Publication No. US2006062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B
; FILE REFERENCE: PP523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21

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PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 3239
 SEQ ID NO: 919
 LENGTH: 249
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-266-444-919

Query Match Similarity 79.5%; Score 534.5; DB 11; Length 249;
 Best Local Similarity 81.7%; Pred. No. 1.3e-41;
 Matches 103; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 QVQLQSGAEVKPGASVKVSKASGTYPTSDINWROATQGGLEMWGWINPNSGNTDY 60
 Db 1 AQKFQGRVMTRDTISIATMELSSRSEDTAIYCVR-GFGRSYNYDYYGMDWQGT 119

Qy 61 AQKFQGRVMTRDTISIATMELSSRSEDTAIYCVR-GFGRSYNYDYYGMDWQGT 60
 Db 61 AQKFQGRVMTRDTISIATMELSSRSEDTAIYCVR-GFGRSYNYDYYGMDWQGT 119

Qy 120 TTVVSS 125
 Db 121 TTVVSS 126

RESULT 112-917-110
 US-11-211-917-110
 ; Sequence 110, Application US/11211917
 ; Publication No. US20060093600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BEDIAN, VAHE
 ; APPLICANT: GLADIAN, RONALD P.
 ; APPLICANT: CORVALAN, JOSE
 ; APPLICANT: JIA, XIAO-CHI
 ; APPLICANT: FENG, XIAO
 ; TITLE OF INVENTION: ANTIBODIES TO CD40
 ; FILE REFERENCE: ABX-PP/3 US
 ; CURRENT APPLICATION NUMBER: US/11/211,917
 ; PRIORITY FILING DATE: 2005-08-25
 ; PRIOR APPLICATION NUMBER: 60/348,980
 ; PRIORITY FILING DATE: 2001-11-09
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 110
 ; LENGTH: 122
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-211-917-110

Query Match Similarity 78.5%; Score 527.5; DB 10; Length 122;
 Best Local Similarity 79.4%; Pred. No. 2.9e-41;
 Matches 102; Conservative 7; Mismatches 10; Indels 9; Gaps 2;

Qy 1 QVQLQSGAEVKPGASVKVSKASGTYPTSDINWROATQGGLEMWGWINPNSGNTDY 60
 Db 1 QVQLQSGAEVKPGASVKVSKASGTYPTSDINWROATQGGLEMWGWINPNSGNTDY 60

Qy 61 AQKFQGRVMTRDTISIATMELSSRSEDTAIYCVR-GFGRSYNYDYYGMDWQGT 117
 Db 61 AQKFQGRVMTRDTISIATMELSSRSEDTAIYCVR-GFGRSYNYDYYGMDWQGT 114

Qy 118 GTTVVSS 125
 Db 119 GTLVVSS 122

RESULT 113-515-1896
 US-11-054-515-1896
 ; Sequence 1896, Application US/11054515
 ; Publication No. US2005025532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENT IN RELEASE #1.0, VERSION #1.30 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/834,397
 FILING DATE: 29-APR-2004
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,324
 FILING DATE: 24-JAN-2000
 APPLICATION NUMBER: US/09/025,769
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid

Db 116 ||||:||||| MDVWGKGTMVTVSS 129

Search completed: May 15, 2006, 17:25:50
Job time : 20.8498 secs

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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:59:17 ; Search time 25.2146 Seconds (without alignments)

476.989 Million cell updates/sec

Title: US-10-041-860-48

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKGASVKV.....YDYYGMDVWGQTTVTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	82.9	127	S34014	Ig heavy chain V r
2	517.5	80.0	136	S31600	Ig heavy chain V r
3	53.4	79.5	129	S46393	Ig heavy chain V r
4	51.6	76.9	118	S36265	Ig heavy chain V r
5	51.5	76.6	123	S33548	Ig heavy chain V-1
6	51.4	76.5	129	S36260	Ig heavy chain V r
7	51.5	76.1	135	S49350	anti-Sm antibody V
8	510.5	76.0	132	S31596	Ig heavy chain V r
9	500	74.4	131	S26792	Ig heavy chain V r
10	499	74.3	119	PH0961	Ig heavy chain V r
11	496.5	73.9	110	PH1670	Ig heavy chain V r
12	496	73.8	98	S26918	Ig heavy chain V r
13	493.5	73.7	132	PH0954	Ig heavy chain V r
14	495	73.7	171	S22623	Ig heavy chain V r
15	496.5	73.6	118	PH1666	Ig heavy chain V r
16	493.5	73.4	136	PH0960	Ig heavy chain V r
17	488	72.7	143	E1R9UD	Ig heavy chain pre
18	498	72.6	127	PH0955	Ig heavy chain V r
19	487.5	72.5	124	S19665	Ig heavy chain V r
20	486	72.3	133	C31548	Ig heavy chain V-1
21	486	72.3	627	S14683	Ig mu chain precursor
22	484	72.0	142	A32483	Ig heavy chain V r
23	480	71.4	122	S36271	Ig heavy chain V r
24	490	71.4	160	PL0105	anti-PR2 erythrocy
25	477.5	71.1	126	B33548	Ig heavy chain V-1
26	476.5	70.9	114	PH1667	Ig heavy chain V r
27	473.5	70.5	128	PH0952	Ig heavy chain V r
28	472.5	70.3	120	S31999	Ig heavy chain V r
29	468	69.6	109	PH1668	Ig heavy chain V r

ALIGNMENTS

RESULT 1									
S34014	Ig heavy chain V region - human	C;Species: Homo sapiens (man)	C;Date: 02-Dec-1993 #Sequence_revision 10-Nov-1995 #text_change 16-Aug-1996	C;Accession: S34014; S30335	R;Marlette, X.; Tsapis, A.; Brouet, J. C.	Bur. J. Immunol. 123, 846-851, 1993	A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal antibodies. A;Reference number: S34001; PMID:7681398	A;Accession: S34014	A;Status: Preliminary
		A;Molecule type: mRNA	A;Residues: 1-127 <MAR>						
		A;Cross-references: UNIPARC:UPI000176D1; EMBL:Z18321	C;Superfamily: immunoglobulin V region; immunoglobulin homology						
		C;Keywords: heterotrimer; immunoglobulin F15-98/Domain: immunoglobulin homology <IMM>							
		Query Match	82.9%	Score 557; DB 2; Length 127;					
		Best Local Similarity	82.1%	Pred. No. 1.4e-42;					
		Matches 105; Conservative 10; Mismatches 10; Indels 2; Gaps 1;							
Qy	1 QYQLVOSGAEVYKKPGASVKVSKAGSGYTFSYDIAVYCVR--GFGYKSYNDYVYGMVYQGLERMGWGMWNPNSGRTDY 60	Db	1 QYQMVGSGAEVYKKPGASVKVSKAGSGYTFSYDIAVYCVR--GFGYKSYNDYVYGMVYQGLERMGWGMWNPNSGRTGY 60						
Qy	61 AOKFQGRVMTRDTISIATMBSLSSRSEDTAIYCVR--GFGYKSYNDYVYGMVYQGLERMGWGMWNPNSGRTDY 118	Db	61 AOKFQGRVMTRDTISIATMBSLSSRSEDTAIYCVR--GFGYKSYNDYVYGMVYQGLERMGWGMWNPNSGRTGY 120						
Qy	119 TTVYSS 125	Db	121 TTVYSS 127						

R;Cuisinier, A.M.; Gauthier, L.; Boubli, M.; Tonnelle, C.

C;Accession: S31600

C;Description: Submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31595

A;Accession: S31600

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-136 <CU1>

A;Cross-references: UNIPARC:UPI000116453; EMBL:Z14165; PMID:930994

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin homology <IMM>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match Score 537.5; DB 2; Length 136;

Best Local Similarity 80.0%; Pred. No. 8.1e-41;

Matches 103; Conservative 6; Mismatches 7; Indels 9; Gaps 1;

Qy 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60

Db 20 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 79

Qy 61 AQKFGQRTVMTRDTISIATAMELSSRLSRTDAIYCYCVRGFGSYNNDDYTGMDVQGQRT 120

Db 80 AQKFGQRTVMTRDTISIATAMELSSRLSRTDAIYCYCVRGFGSYNNDDYTGMDVQGQRT 130

Qy 121 VTVSS 125

Db 131 VTVSS 135

Db 114 VTVSS 118

RESULT 3

S4 6393

19 heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000

C;Accession: S46393

R;Pigini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

C;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A;Reference number: S46390; MUID:94254092; PMID:8196048

A;Accession: S46393

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-129 <FIG>

A;Cross-references: UNIPARC:UPI000011663A; EMBL:231680; PIDN:CAA83485.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin homology <IMM>

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match Score 534; DB 2; Length 129;

Best Local Similarity 79.8%; Pred. No. 1.6e-40;

Matches 103; Conservative 7; Mismatches 15; Indels 4; Gaps 1;

Qy 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60

Db 1 QVQLVSGAELYKPGASVKVSKASGYFTSYDINVRQATGQGLEWMGWINPNSGNTDY 60

Qy 61 AQKFGQRTVMTRDTISIATAMELSSRLSRTDAIYCYCVRGFGSYNNDDYTGMDVQGQRT 119

Db 61 AQKFGQRTVMTRDTISIATAMELSSRLSRTDAIYCYCVRGFGSYNNDDYTGMDVQGQRT 117

Qy 117 QGTTVTVSS 125

Db 121 KGTTVTVSS 129

Db 118 LTVSS 123

RESULT 4

S3 6265

19 heavy chain V region (clone alpha-MUCL-1) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C;Accession: S36265

R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A;Title: Human anti-self antibodies with high specificity from phage display libraries.

A;Reference number: S36256; MUID:93178448; PMID:7679990

A;Accession: S36265

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-129 <GR>

A;Cross-references: UNIPARC:UPI00001180DB; EMBL:218851; MUID:933124; PIDN:CAA79303.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Best Local Similarity 79.2%; Pred. No. 1.9e-38; Matches 99; Conservative 6; Mismatches 7; Indels 13; Gaps 1;											
Query Match Score 514; DB 2; Length 129; Best Local Similarity 76.5%; Pred. No. 9.3e-19; Matches 101; Conservative 8; Mismatches 16; Indels 4; Gaps 2; Matches 101; Conservative 8; Mismatches 16; Indels 4; Gaps 2;	Qy	1 QVQLVQSGAEVYKPGASVKVSCKASGYTFTSYDINWVROATQGLEMWGMINPNSGNTDY 60	Qy	1 QVQLVQSGAEVYKPGASVKVSCKASGYTFTSYDINWVROATQGLEMWGMINPNSGNTDY 60	Db	20 QVQLVQSGAEVYKPGASVKVSCKASGYTFTSYDINWVROATQGLEMWGMINPNSGNTDY 79	Db	1 QVQLVQSGAEVYKPGASVKVSCKASGYTFTSYDINWVROATQGLEMWGMINPNSGNTDY 60	Db	20 QVQLVQSGAEVYKPGASVKVSCKASGYTFTSYDINWVROATQGLEMWGMINPNSGNTDY 79	
Db	1 QVQLVQSGAEVYKPGASVKVSCKASGYTFTSYDINWVROATQGLEMWGMINPNSGNTDY 60	Db	1 QVQLVQSGAEVYKPGASVKVSCKASGYTFTSYDINWVROATQGLEMWGMINPNSGNTDY 60	Qy	61 AQKPGQRTVMTRDTTS1STAYMELSS1RS6TAAIYCYCR-GFGSYNDDY-YYGMDWVG 116	Qy	61 AQKPGQRTVMTRDTTS1STAYMELSS1RS6TAAIYCYCR-GFGSYNDDY-YYGMDWVG 116	Db	80 AQKPGQRTVMTRDTTS1STAYMELSS1RS6TAAIYCYCR-GFGSYNDDY-YYGMDWVG 120	Db	80 AQKPGQRTVMTRDTTS1STAYMELSS1RS6TAAIYCYCR-GFGSYNDDY-YYGMDWVG 120
Qy	61 AQKPGQRTVMTRDTTS1STAYMELSS1RS6TAAIYCYCR-GFGSYNDDY-YYGMDWVG 116	Db	61 AQKPGQRTVMTRDTTS1STAYMELSS1RS6TAAIYCYCR-GFGSYNDDY-YYGMDWVG 120	Qy	121 VTVSS 125	Qy	121 VTVSS 125	Db	127 VTVSS 131	Db	127 VTVSS 131
Qy	117 QSTTVTVSS 125	Db	121 KGTTVTVSS 129	RESULT 9 S26792							
Ig heavy chain V region - human											
C;Species: Homo sapiens (man)											
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000											
C;Accession: S26792											
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.											
Bur. J. Immunol. 22, 241-252, 1992											
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam											
A;Reference number: S26786; PMID:9211632; PMID:1730251											
A;Accession: S26792											
A;Status: preliminary											
A;Molecule type: mRNA											
A;Residues: 1-131 <MOR>											
A;Cross-references: UNIPARC:UPI000115FC3; EMBL:K61012; PIDN:932804; PMID:CAA43346.1; PI											
C;Superfamily: immunoglobulin V region; immunoglobulin homology											
F;15-98/Domain: immunoglobulin											
Query Match Score 500; DB 2; Length 131;											
Best Local Similarity 74.4%; Pred. No. 1.6e-37; Matches 95; Conservative 13; Mismatches 17; Indels 6; Gaps 2;											
Query Match Score 500; DB 2; Length 131;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 511.5; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
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Query Match Score 514; DB 2; Length 135;											
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Query Match Score 514; DB 2; Length 135;											
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Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514; DB 2; Length 135;											
Best Local Similarity 76.1%; Pred. No. 1.6e-38; Matches 100; Conservative 79; Indels 11; Gaps 2; Matches 100; Conservative 79; Indels 11; Gaps 2;											
Query Match Score 514											

F;51-67/Region: complementarity-determining 2
 F;68-98/Region: framework 3
 F;99-107/Region: complementarity-determining 3

Query Match 74.3% Score 499; DB 2; Length 119;
 Best Local Similarity 79.2%; Pred. No. 1.8e-37;
 Matches 99; Conservative 6; Mismatches 14; Indels 6; Gaps 1;

Qy 1 QVQLVQSGAEVKPGASVKSCKASGYTFSYDINWROTQGLEYWGMWNPNSGNTDY 60
 Db 1 QVQLVQSGAEVKPGASVKSCKASGYTFSYDINWROTQGLEYWGMWNPNSGNTGY 60

Qy 61 AQKPGQRVITMTRDTISIATAMELSSRLSERTAIVYCVR 98
 Db 61 AQKPGQRVITMTRDTISIATAMELSSRLSERTAIVYCAR 98

RESULT 13
 PH0954
 Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)

C;Species: Homo sapiens (man)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C;Accession: PH0954
 R;Martin, T.; Duffy, S.P.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A;Title: Evidence for somatic selection of natural autoantibodies.
 A;Reference number: PH0552; MUID:92202880; PMID:1552291

A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-132 <MAR>
 A;Cross-references: UNIPARC:UPI000176CD8
 C;SuperFamily: immunoglobulin V region immunoglobulin homology
 R;Hillson, J.L.; Karr, N.S.; Oppiliger, I.R.; Mannik, M.; Sasso, B.H.
 J. Exp. Med. 178, 331-336, 1993
 A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A. Reference number: PH1642; MUID:93301610; PMID:8315388
 A;Accession: PH1670
 A;Molecule type: mRNA
 A;Residues: 1-110 <HL>
 A;Cross-references: UNIPARC:UPT0000176BBB
 A;Experimental source: B cell
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;7-90/Region: immunoglobulin homology <IMM>

Query Match 73.9% Score 496.5; DB 2; Length 110;
 Best Local Similarity 82.1%; Pred. No. 2.8e-37;
 Matches 96; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

Qy 9 AEVKKGASVKSCKASGYTFSYDINWROTQGLEYWGMWNPNSGNTDYAQKPGRY 68
 Db 1 AEVKKGASVKSCKASGYTFSYDINWROTQGLEYWGMWNPNSGNTGYAQKPGRY 60

Qy 69 TMTRDTISIATAMELSSRLSERTAIVYCVR 98
 Db 61 TMTRDTISIATAMELSSRLSERTAIVYCAR-GKGGBF----DIWQQTLYVSS 110

RESULT 14
 S23623
 Ig heavy chain V region precursor - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C;Accession: S23623
 R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
 A;Reference number: S2021117; PMID:1404388
 A;Accession: S22918
 A;Molecule type: DNA
 A;Residues: 1-98 <OM>
 A;Cross-references: UNIPARC:UPI0000115593; EMBL:K59702; PIDN:CAA78187.1; PID
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;34-117/Region: immunoglobulin homology <IMM>

Query Match 73.8% Score 496; DB 2; Length 98;

Query Match 73.7%; Score 495.5; DB 2; Length 171;
 Best Local Similarity 70.9%; Pred. No. 5.5e-37; Gaps 2;
 Matches 95; Conservative 9; Mismatches 13; Indels 17; Gaps 2;

Qy 1 QVQLVQSGAEVKCPGASVKVSKASGVTSYDINWVROATGGLEMGWIPNSGNTDY 60
 Db 20 QVQLVQSGAEVKCPGASVKVSKASGVTSYDINWVROATGGLEMGWIPNSGNTDY 79

Qy 61 AQKFQGRVTTMRTDTISIATAYMELSLSLRBDTALIYCYRGFGSYNDYIG----- 111
 Db 80 GQKFQGRVTTMRTDTISIATAYMELSLSLRDTAVYYCA-----1EYFYDSDLXPSDV 131

Qy 112 MDYWGQGTIVTVSS 125

Db 132 FDIWGQTMVTVSS 145

RESULT 15

PHI1666
 Ig heavy chain V region (clone 6C9) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C;Accession: PHI1666
 R;Hillison, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Sasso, E.H.
 J;Exp. Med. 178, 331-336, 1993
 A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
 A;Reference number: PHI1642; MUID:93301610; PMID:8315388
 A;Accession: PHI1666
 A;Molecule type: mRNA
 A;Residues: 1-118 <HIL>
 A;Cross-references: UNIPARC:UPI0000176BE7
 A;Experimental source: B cell
 C;Superfamily: immunoglobulin V region; immunoglobulin
 F;Keywords: heterotetramer; immunoglobulin
 P;7-90/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 494.5; DB 2; Length 118;
 Best Local Similarity 80.5%; Pred. No. 4.5e-37; Gaps 1;
 Matches 95; Conservative 6; Mismatches 16; Indels 1; Gaps 1;

Qy 9 AEVKKPGASVKVSKASGVTSYDINWVROATGGLEMGWIPNSGNTDYAQKFQGRV 68
 Db 1 AEVKKPGASVKVSKASGVTSYDINWVROATGGLEMGWIPNSGNTDYAQKFQGRV 60

Qy 69 TMTRDTSTIATAYMELSLRDTAVYYCAVTDGG1KFYYYGMWDQGTTTVSS 125
 Db 61 TMTRDTSAATAYMELSLRDTAVYYCAVTDGG1KFYYYGMWDQGTTTVSS 118

Search completed: May 15, 2006, 17:04:50
 Job time : 26.2146 secs

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBITaxonID=9606;
RN [1] NUCLEOTIDE SEQUENCE.
RX MEDLINE=83005234; PubMed=6816565;
RA Kenten J.H., Moijgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RN "Cloning and sequence determination of the gene for the human
immunoglobulin epsilon chain expressed in a myeloma cell line.";
RN [2] PROTEIN SEQUENCE OF 20-147;
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (Eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: This epsilon chain was isolated from a myeloma
protein.
-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
DR HSSP; P01751; INGB;
DR GO; GO-0005516; C:extracellular region; NAS.
DR GO; GO-0003823; F:antigen binding; NAS.
DR GO; GO-0006555; F:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; Ig_v.
DR PROSITE; PSS0835; Ig_LIKE;
DR PROSITE; PSS0835; Ig_LIKE;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid; Signal.
PT SIGNAL
FT CHAIN 1 19
FT DOMAIN 20 147 Ig heavy chain V-I region ND.
FT MOD_RES 20 131 Ig-like.
FT DISULFID 41 20 Pyrrolidone carboxylic acid.
FT CONFLICT 21 21 T -> V (in Ref. 2).
FT CONFLICT 53 54 IH -> HI (in Ref. 2).
FT CONFLICT 67 68 VG -> GV (in Ref. 2).
FT CONFLICT 125 125 Missing (in Ref. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

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Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

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Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

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Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

Query Match 72.7%; Score 488.5; DB 1; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.3e-10; Indels 3; Gaps 1;

Matches 90; Conservative 90; Mismatches 19; Indels 3; Gaps 1;

Sequence 147 AA; 16496 MW; 948P9F72A5366C20 CRC64;

DR	Pfam; PF07654; C1-set; 2.
DR	SMART; SM00409; IG; 4.
SMART;	SM00407; IgCl; 3.
SMART;	SM00406; IgV; 1.
DR	PROSITE; PS00230; Ig MHC; UNKNOWN_2.
KW	Hypothetical protein.
NON TBR	1 MW; 40B3208A84E03B46 CRC64;
FT	1 AA; 54125 MW; 40B3208A84E03B46 CRC64;
SEQUENCE	498 AA; 1
Query Match	Score 71.2%; Score 478.5%; DB 2; Length 498;
Best Local Similarity	74.6%; Pred. No. 5e-39;
Matches	11; Mismatches 18; Indels 3; Gaps 2;
QY	1 QVQLVQSGAEVTKPGASVKVSKASGTYTFTSYDINWVQATCGLEMGWNPNSGNTDY 60
DB	35 QVQLVQSGADYTKPGASVKVSKASGTYTFTSYDINWVQATCGLEMGWNPNSGNTDY 94
QY	61 AQKFGQFVMTMRTDSI STAYMELLSRSSEDPAIYVCTR-GFGSYNNDYXGMDWVGQFT 119
DB	95 AQRFGQFVMTMRTDSI STAYMELLSRSSEDPAIYVCTR-GFGSYNNDYXGMDWVGQFT 152
QY	120 TTVVSS 125
DB	153 LTVVSS 158
RESULT 8	Q8WV24 HUMAN PRELIMINARY;
AC	Q8WV24_HUMAN PRELIMINARY;
AC	Q8WV24;
RA	Zheng S.; Shao X.; Cao J.; Geng L.; Fang Y.; Dong Q.;
DR	Submitted (JUN-2001) to the ENB/GenBank/DBJ databases.
DR	01-MAR-2002 (T-EMBLrel. 20, Created)
DR	01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DR	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DR	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
OC	Homo sapiens (Human).
NCBI_TAXID=9605;	
RN	NUCLEOTIDE SEQUENCE.
RP	NUCLEOTIDE SEQUENCE.
RA	Zheng S.; Shao X.; Cao J.; Geng L.; Fang Y.; Dong Q.;
DR	Submitted (JUN-2001) to the ENB/GenBank/DBJ databases.
DR	EMBL; AF283666; AAL56987.1; -; mRNA.
DR	HSSP; P01876; IOW0.
DR	SMART; Q8WV24; 267-475.
DR	InterPro; IPR00110; Ig-like.
DR	InterPro; IPR00597; Ig-cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; C1-set; 2.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS00835; Ig_LIKE; 4.
DR	PROSITE; PS00296; Ig_MHC; UNKNOWN_1.
KW	Immunoglobulin domain; Repeat.
SEQUENCE	497 AA; 53666 MW;
QY	1 QVQLVQSGAEVTKPGASVKVSKASGTYTFTSYDINWVQATCGLEMGWNPNSGNTDY 60
DB	20 QEQLEQSGAEVTKPGASVKVSKASGTYTFTSYDINWVQATCGLEMGWNPNSGNTDY 79
QY	61 AQKFGQFVMTMRTDSI STAYMELLSRSSEDPAIYVCTR-----GFGSYNNDYXGMDWVGW 115
DB	80 AQKFGQFVMTMRTDSI STAYMELLSRSSEDPAIYVCTR-----GFGSYNNDYXGMDWVGW 134
QY	116 GQGTVVSS 125
DB	135 GHGTIVVSS 144
Query Match	Score 70.5%; Score 474; DB 2; Length 497;
Best Local Similarity	70.1%; Pred. No. 1.4e-38;
Matches	13; Mismatches 16; Indels 10; Gaps 2;
QY	1 QVQLVQSGAEVTKPGASVKVSKASGTYTFTSYDINWVQATCGLEMGWNPNSGNTDY 60
DB	20 QEQLEQSGAEVTKPGASVKVSKASGTYTFTSYDINWVQATCGLEMGWNPNSGNTDY 79
QY	61 AQKFGQFVMTMRTDSI STAYMELLSRSSEDPAIYVCTR-----GFGSYNNDYXGMDWVGW 115
DB	80 AQKFGQFVMTMRTDSI STAYMELLSRSSEDPAIYVCTR-----GFGSYNNDYXGMDWVGW 134
QY	1 QVQLVQSGAEVTKPGASVKVSKASGTYTFTSYDINWVQATCGLEMGWNPNSGNTDY 60
DB	20 QVHLVQSGAEVMSFGASVRSVCKSGYAFHTSYIWRQPGQGLEWMGNTIPS SSSDNTRF 7
QY	61 AQKFGQFVMTMRTDSI STAYMELLSRSSEDPAIYVCTR-----GFGSYNNDYXGMDWVGW 1
DB	80 AKKFGQFVMTMRTDSI STAYMELLSRSSEDPAIYVCTR-----GFGSYNNDYXGMDWVGW 1
Query Match	Score 70.0%; Score 470.5%; DB 2; Length 500;
Best Local Similarity	71.9%; Pred. No. 3.1e-38;
Matches	92; Conservative 11; Mismatches 22; Indels 3; Gaps
QY	1 QVQLVQSGAEVTKPGASVKVSKASGTYTFTSYDINWVQATCGLEMGWNPNSGNTDY 60
DB	20 QVHLVQSGAEVMSFGASVRSVCKSGYAFHTSYIWRQPGQGLEWMGNTIPS SSSDNTRF 7

RESULT 15	
Q6P089 15 HUMAN	PPT; 480 AA.
Q6P089; HUMAN PRELIMINARY;	
AC	
DT 05-JUL-2004 (TREMBLrel. 27, Created)	
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
DE Hypothetical protein.	
OS Homo sapiens (Human).	
OC Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	
OC NCBI_TaxID:9606;	
OX [1] -	
RN NUCLEOTIDE SEQUENCE	
RP TISSUE=Glandular pool-thyroid;	
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RX STRMberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.P., Bhat N.K., Altschul S.P., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.P., Jordan H., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Usdin T.B., Tashiroki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullaya S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villarhon D.K., Murthy D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Homan E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalak U., Shailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marrs M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	

Query	Subject	Sequence	Score	Length	Match	Mismatches	Gaps
[2]	RRN	NUCLEOTIDE SEQUENCE.					
	RRP	TISSUE=Glandular pool- thyroid;					
	RC	Strasburg, R.;					
	RA	Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.					
	RL	EMBL; BCO5733; ARH65733.1; -; mRNA.					
	RR	HSSP; P01751; 1A5W.					
	RRD	SNR; Q65089; 250_458.					
	RRD	InterPro; IPR003559; Ig.					
	RRD	InterPro; IPR007110; Ig-like.					
	RRD	InterPro; IPR003587; Ig cl.					
	RRD	InterPro; IPR03006; Ig_MHC.					
	RRD	InterPro; IPR003596; Ig_v.					
	RRD	PFAM; PF07654; Cl-set; 2.					
	RRD	SMART; SM00439; Ig; 4.					
	RRD	SMART; SM00407; IgC1; 3.					
	RRD	PROSITE; PSS0835; Ig_LIKE; 4.					
	RRD	PROSITE; PS00290; Ig_MHC; UNKNOWN_2.					
	RRD	Hypothetical protein.					
	RRD	SEQUENCE 480 AA; 51.997 MW;					
	RRD	2B286C57B4F0ED65 CRC64;					
	Query Match	65.2%; Score 438; DB 2; Length 480;					
	Best Local Similarity	68.5%; Pred. No. 5_2e-35;					
	Matches	87; Conservative 13; Mismatches 19; Indels 8; Gaps					
Qy	1	QYVOLVQSGAEVKKEPGASVVKSVCKASGTVTSDINWYRQATQCGLEKMGWNPNSGNTDY	6				
Ddb	20	QVQEVQSGAEVKKEPGASVVKSVCKASGTVTSDINWYRQATQCGLEKMGWNPNSGNTDY	7				
Qy	61	AQKQGRGTVITMRTDTSITAMMELSSLRSRDTIAYKTCRGFG-YISKMYDITYGMDWQGQ	1				
Ddb	80	AEXQGRGTVITIOTSLNTAYMELTSLSDDTAYLTYCARGHSWSSSTYFDY-----WGQG	1				
		119 TTVTVSS 125					

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Qy	1	BIVLTQSPGTLSSLGERATLSCRAQSQVSSSTLAWYQOKPGQAPRILLYATSSRATGIP	60
Db	1	BIVLTQSPGTLSSLGERATLSCRAQSQVSSSTLAWYQOKPGQAPRILLYATSSRATGIP	60
Qy	61	DRFGSGSGCTDFTLTLTSLRLEPDFAVYCCQYGSSPCSFGQGKWLKIK	108
Db	61	DRFGSGSGCTDFTLTLTSLRLEPDFAVYCCQYGSSPCSFGQGKWLKIK	108
RESULT 2			
	ADK18951	ADK18951 standard; protein; 108 AA.	
ID	ADK18951	standard; protein; 108 AA.	
XX			
AC	ADK18951;		
XX			
DT	06-MAY-2004	(first entry)	
XX			
DE	Anti-human PDGF-D antibody protein related sequence #177.		
XX			
KW	antinflammatory; immunomodulator; cytostatic; gene therapy.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003057857-A2.		
XX			
PD	17-JUL-2003.		
XX			
PF	06-JAN-2003;	2003WO-US000398.	
XX			
PR	07-JAN-2002;	2002US-00041860.	
XX			
PA	(ABGEE-) ABGENIX INC.		
XX			
PI	Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;		
PI	Bezzbeh B;		
XX			
DR	WPI; 2003-587119/55.		
XX			
PT	New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.		
PT			
PT	Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188-0.9 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid PCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.		
XX			
SQ	Sequence 108 AA:		
Qy	1	BIVLTQSPGTLSSLGERATLSCRAQSQVSSSTLAWYQOKPGQAPRILLYATSSRATGIP	60
Db	1	BIVLTQSPGTLSSLGERATLSCRAQSQVSSSTLAWYQOKPGQAPRILLYATSSRATGIP	60
Qy	61	DRFGSGSGCTDFTLTLTSLRLEPDFAVYCCQYGSSPCSFGQGKWLKIK	108
Db	61	DRFGSGSGCTDFTLTLTSLRLEPDFAVYCCQYGSSPCSFGQGKWLKIK	108
Qy	61	DRFGSGSGCTDFTLTLTSLRLEPDFAVYCCQYGSSPCSFGQGKWLKIK	108
Db	61	DRFGSGSGCTDFTLTLTSLRLEPDFAVYCCQYGSSPCSFGQGKWLKIK	108

RESULT 3		RESULT 4	
ADKL8835	ID ADKL8835 standard; protein; 108 AA.	ADKL8801	ID ADKL8801 standard; protein; 108 AA.
XX	AC ADKL8835;	XX	AC ADKL8801;
XX	DT 06-MAY-2004 (first entry)	XX	DT 06-MAY-2004 (first entry)
XX	DE Anti-human PDGF-D antibody protein related sequence #61.	XX	DE Anti-human PDGF-D antibody protein related sequence #27.
XX	KW antiinflammatory; immunomodulator; cytostatic; gene therapy.	XX	KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX	OS Homo sapiens.	XX	OS Homo sapiens.
XX	PN WO2003057857-A2.	XX	PN WO2003057857-A2.
XX	PD 17-JUL-2003.	XX	PD 17-JUL-2003.
XX	PP 06-JAN-2003; 2003WO-US000398.	XX	PP 06-JAN-2003; 2003WO-US000398.
XX	PR 07-JAN-2002; 2002US-00041860.	XX	PR 07-JAN-2002; 2002US-00041860.
XX	PA (ABG-1) ABGENIX INC.	XX	PA (ABG-1) ABGENIX INC.
XX	PI Coryalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Bezabeh B;	XX	PI Coryalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Bezabeh B;
XX	DR WPI; 2003-587119/55.	XX	DR WPI; 2003-587119/55.
XX	PT New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.	XX	PT New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D). The antibody is useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
XX	PS Disclosure: SEQ ID NO 259; 255pp; English.	XX	PS Disclosure: SEQ ID NO 259; 255pp; English.
XX	CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibody is useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer. The antibody is useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) generated using an active protein fragment of the gene product clone 3064188.0.99 arising in the conditioned medium obtained from HEK293 cells are transfected with the plasmid pCEP4/Sec-3066. Sequence corresponds to a protein used in the invention.	CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibody is useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer. The antibody is useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) generated using an active protein fragment of the gene product clone 3064188.0.99 arising in the conditioned medium obtained from HEK293 cells are transfected with the plasmid pCEP4/Sec-3066. Sequence corresponds to a protein used in the invention.	
XX	SQ Sequence 108 AA;	XX	SQ Sequence 108 AA;
XX	Query Match 100.0%; Score 558; DB 7; Length 108;	XX	Query Match 100.0%; Score 558; DB 7; Length 108;
XX	Best Local Similarity 100.0%; Pred. No. 4.1e-35;	XX	Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 108;	Matches 0; Mismatches 0; Indels 0;	Matches 108;	Matches 0; Mismatches 0; Indels 0;
Qy 1 EIVLTQSPGTLSIISPGERATLSSCRASGSVSSSYLAWYQQKPGQAPRLLIYAA	Qy 1 EIVLTQSPGTLSIISPGERATLSSCRASGSVSSSYLAWYQQKPGQAPRLLIYAA	Qy 1 EIVLTQSPGTLSIISPGERATLSSCRASGSVSSSYLAWYQQKPGQAPRLLIYAA	Qy 1 EIVLTQSPGTLSIISPGERATLSSCRASGSVSSSYLAWYQQKPGQAPRLLIYAA
Db 1 EIVLTQSPGTLSIISPGERATLSSCRASGSVSSSYLAWYQQKPGQAPRLLIYAA	Db 1 EIVLTQSPGTLSIISPGERATLSSCRASGSVSSSYLAWYQQKPGQAPRLLIYAA	Db 1 EIVLTQSPGTLSIISPGERATLSSCRASGSVSSSYLAWYQQKPGQAPRLLIYAA	Db 1 EIVLTQSPGTLSIISPGERATLSSCRASGSVSSSYLAWYQQKPGQAPRLLIYAA
Qy 61 DRFGSGSGTGTDFPLTISRLPEPDFAVYTCQQYGSSPCSFGQGTPLKIEK 10	Qy 61 DRFGSGSGTGTDFPLTISRLPEPDFAVYTCQQYGSSPCSFGQGTPLKIEK 10	Qy 61 DRFGSGSGTGTDFPLTISRLPEPDFAVYTCQQYGSSPCSFGQGTPLKIEK 10	Qy 61 DRFGSGSGTGTDFPLTISRLPEPDFAVYTCQQYGSSPCSFGQGTPLKIEK 10
Db 61 DRFGSGSGTGTDFPLTISRLPEPDFAVYTCQQYGSSPCSFGQGTPLKIEK 10	Db 61 DRFGSGSGTGTDFPLTISRLPEPDFAVYTCQQYGSSPCSFGQGTPLKIEK 10	Db 61 DRFGSGSGTGTDFPLTISRLPEPDFAVYTCQQYGSSPCSFGQGTPLKIEK 10	Db 61 DRFGSGSGTGTDFPLTISRLPEPDFAVYTCQQYGSSPCSFGQGTPLKIEK 10

KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 OS Homo sapiens.
 XX WO2003057857-A2.
 XX 17-JUL-2003.
 XX 06-JAN-2003; 2003WO-US000398.
 XX 07-JAN-2002; 2002US-00041860.
 XX (AEGE-) ABGENIX INC.
 PI Corvalan JRP, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;
 Bezabeh B;
 DR WPI; 2003-587119/55.
 XX New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
 Disclosure: SEQ ID NO 225; 255pp; English.
 The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to Platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid PCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
 Sequence 108 AA;

Query Match 100.0%; Score 558; DB 7; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.1e-35;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSTYQKPGQAPRILYATSSRATGIP 60
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSTYQKPGQAPRILYATSSRATGIP 60
 Qy 61 DRFGSGSGTGTDTLTLTSLRLEPDFAVYQCGYGSPLCSFGQGTKLK 108
 Db 61 DRFGSGSGTGTDTLTLTSLRLEPDFAVYQCGYGSPLCSFGQGTKLK 108

RESULT 5
 ADL25394 standard; protein; 108 AA.
 XX AC ADL25394;
 XX DT 17-JUN-2004 (first entry)
 Human mAb 6.4 light chain variable region protein SEQ ID NO: 4.
 XX antibody; binding fragment; platelet derived growth factor-**DD**; PDGF-**DD**; nephritis; mesangial cell proliferation inhibition;
 KW mesangial proliferative glomerulonephritis; nephrotropic;
 KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;
 KW gene therapy; human; monoclonal antibody; mAb.
 XX Homo sapiens.
 XX PN WO2004024038-A2.
 XX PD 25-MAR-2004.
 XX PR 15-JUL-2003; 2003US-0487431P.
 XX PA (AMGE-) AMGEN INC.

PP 16-SEP-2003; 2003WO-US029414.
 XX 16-SEP-2002; 2002US-0411137P.
 XX (ABGB-) ABGENIX INC.
 PA (CTRA-) CURAGEN CORP.
 XX PI Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;
 XX DR WPI; 2004-269881/25.
 XX PT Use of an antibody or its binding fragment that binds platelet derived growth factor-**DD** (PDGF-**DD**) for preparing a medicament for treating nephritis.
 XX Disclosure: SEQ ID NO 4; 115pp; English.
 XX The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-**DD** (PDGF-**DD**), where the antibody is useful in preparing a medicament for treating nephritis. Also described:
 CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
 CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antiinflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-**DD**, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the exemplification of the present invention.
 Sequence 108 AA;

Query Match 100.0%; Score 558; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.1e-35;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSTYQKPGQAPRILYATSSRATGIP 60
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSTYQKPGQAPRILYATSSRATGIP 60

Qy 61 DRFGSGSGTGTDTLTLTSLRLEPDFAVYQCGYGSPLCSFGQGTKLK 108
 Db 61 DRFGSGSGTGTDTLTLTSLRLEPDFAVYQCGYGSPLCSFGQGTKLK 108

RESULT 6
 ADY26769 standard; protein; 108 AA.
 XX AC ADY26769;
 XX DT 19-MAY-2005 (first entry)
 XX Anti-NGF-antibody light chain variable region SEQ ID NO 84.
 XX Homo sapiens.
 XX KW analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
 KW neurotrophic disease; NGF; nerve growth factor.
 XX KW light chain variable region.
 OS WO2005019266-A2.
 PN XX
 PD 03-MAR-2005.
 XX PP 15-JUL-2004; 2004WO-US022876.
 XX PR 15-JUL-2003; 2003US-0487431P.
 XX PA (AMGE-) AMGEN INC.

PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;
 XX DR, WPI, 2005-202606/21.

XX New human anti-nerve growth factor (NGF) neutralizing antibodies useful for manufacturing a medicament for treating painful disorders (e.g. acute pain) or conditions associated with increased expression or sensitivity to NGF.

XX PS SEQ ID NO 84; 190pp; English.

XX The invention describes an isolated human antibody that interacts with or binds specifically to human nerve growth factor (NGF) and neutralize the function of NGF. Also described are: methods of treating a condition caused by increased expression of NGF or increased sensitivity to NGF in a patient; methods for detecting NGF in a biological sample; an NGF specific binding agent comprising any of the 59 amino acid sequences comprising, for e.g., 123, 107 or 14 amino acids, as mentioned in the specification, and where the binding agent can bind to NGF; a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of the antibody or binding agent cited above; or a medicament for treating a painful disorder or condition associated with increased expression of NGF or increased sensitivity to NGF, the medicament comprising a pharmaceutical amount of a monoclonal antibody or its immunologically functional immunoglobulin fragment, or pharmaceutical salts of the monoclonal antibody or the fragment, where the monoclonal antibody is at least one of the monoclonal antibody cited above, and a pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or polynucleotide that encodes the above antibody or binding agent; an isolated cell line that produces the above antibody or binding agent; an expression vector comprising the above polynucleotide; and a host cell comprising the nucleic acid or expression vector. The composition (including the antibody) and methods are useful for manufacturing a medicament for treating a painful disorder (e.g. acute pain, dental pain, or pain from trauma or cancer), or a condition associated with increased expression of NGF or increased sensitivity to NGF. This is the amino acid sequence of a human NGF antibody light chain variable region.

XX Sequence 108 AA;

Query Match 95.9%; Score 535; DB 9; Length 108;
 Best Local Similarity 96.3%; Pred. No. 2.3e-33;
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 EIVLQSPGTLSLSPGERATLSCRASQSSSYLAWYQQKPGQARLLIYATSSRATGIP 60
 1 EIVLQSPGTLSLSPGERATLSCRASQSSSYLAWYQQKPGQARLLIYATSSRATGIP 60

Qy 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSPPCSFGGTKLBIK 108
 Db 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSPPCSFGGTKLBIK 108

Qy 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSPPCSFGGTKLBIK 108
 Db 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSPPCSFGGTKLBIK 108

RESULT 7
 ADY26816 standard; protein; 108 AA.

XX ADY26816;

XX DT 19-MAY-2005 (first entry)

XX Human anti-NGF-antibody light chain SEQ ID NO 131.

XX KW analgesic; gene therapy; antibody engineering; pharmaceutical; pain; neurological disease; NGF; nerve growth factor; light chain.

XX Homo sapiens.

PN WO2005019266-A2.

XX PD 03-MAR-2005.

XX PP 15-JUL-2004; 2004WO-US022876.

XX PR 15-JUL-2003; 2003US-0487431P.

XX PA (AMGEN INC.

XX PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;

XX DR, WPI, 2005-202606/21.

XX PS SEQ ID NO 131; 190pp; English.

XX The invention describes an isolated human antibody that interacts with or binds specifically to human nerve growth factor (NGF) and neutralize the function of NGF. Also described are: methods of treating a condition caused by increased expression of NGF or increased sensitivity to NGF in a patient; methods for detecting NGF in a biological sample; an NGF specific binding agent comprising any of the 59 amino acid sequences comprising, for e.g., 123, 107 or 14 amino acids, as mentioned in the specification, and where the binding agent can bind to NGF; a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of the antibody or binding agent cited above; or a medicament for treating a painful disorder or condition associated with increased expression of NGF or increased sensitivity to NGF, the medicament comprising a pharmaceutical amount of a monoclonal antibody or its immunologically functional immunoglobulin fragment, or pharmaceutical salts of the monoclonal antibody or the fragment, where the monoclonal antibody is at least one of the monoclonal antibody cited above, and a pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or polynucleotide that encodes the above antibody or binding agent; an isolated cell line that produces the above antibody or binding agent; an expression vector comprising the above polynucleotide; and a host cell comprising the nucleic acid or expression vector. The composition (including the antibody) and methods are useful for manufacturing a medicament for the above antibody or binding agent; an isolated cell line that produces the above antibody or binding agent; an expression vector comprising the above polynucleotide; and a host cell comprising the nucleic acid or expression vector. The composition (including the antibody) and methods are useful for manufacturing a medicament for treating a painful disorder (e.g. acute pain, dental pain, or pain from trauma or cancer), or a condition associated with increased expression of NGF or increased sensitivity to NGF. This is the amino acid sequence of a human NGF antibody light chain.

XX Sequence 108 AA;

Query Match 95.9%; Score 535; DB 9; Length 108;
 Best Local Similarity 96.3%; Pred. No. 2.3e-33;
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 EIVLQSPGTLSLSPGERATLSCRASQSSSYLAWYQQKPGQARLLIYATSSRATGIP 60
 1 EIVLQSPGTLSLSPGERATLSCRASQSSSYLAWYQQKPGQARLLIYATSSRATGIP 60

Qy 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSPPCSFGGTKLBIK 108
 Db 61 DRFGSGSSGDTPLTISRLPEDFAVVYQQYGSPPCSFGGTKLBIK 108

RESULT 8
 ADZ57709
 ID ADZ57709 standard; protein; 128 AA.

XX AC ADZ57709;

XX DT 30-JUN-2005 (first entry)

XX Germline antibody A27VKA3.Jk2 light chain protein.

XX KW antibody engineering; cytosstatic; vulnerability; vasotropic; cardiac; monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer; Gastrointestinal ulcer; ischemia; transplant rejection; myocardial infarction; reperfusion injury; restenosis; angioplasty; vascular disease; cancer; retinopathy; endometriosis; arthritis;

XX	Sequence 128 AA;	SG
	Query Match 95.9%; Score 535; DB 9; Length 128;	
	Best Local Similarity 96.3%; Pred. No. 2.7e-33;	
	Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
Qy	1 EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWQQKPCGQAPRLIYATSSRATGIP 60	
Ddb	21 EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWQQKPCGQAPRLIYATSSRATGIP 80	
Qy	61 DRFSGSGSGGTDFTLTLISRLPDEDAYYYCQOYGSSPSFGOCTKLKLTK 108	

compared with yeast genome sequence, showing 71.9% similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the V_k III subgroup gene family. (Updated on 25-MAR-2003 to correct PN field.)

Qy 61 DRPSGSGSGSTDFTLTISRLPEDPAVYCCQXGSSPCSFQGQTCLEIK 108
 Db 81 DRPSGSGSGSTDFTLTISRLPEDPAVYCCQXGSSPCSFQGQTCLEIK 128

RESULT 1.2
 AAM24101
 ID AAM24101 standard; protein; 384 AA.
 XX
 AC AAM24101;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Human EST encoded protein SEQ ID NO: 1626.
 XX
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; Gene mapping; genetic disorder; biodiversity;
 KW gene therapy; nutrition.
 OS Homo sapiens.
 XX
 PN WO200154477-A2.
 XX
 PD 02-AUG-2001.
 XX
 PP 25-JAN-2001; 2001WO-US002687.
 XX
 PR 25-JAN-2000; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-006638870.
 XX
 PA (HYSEQ INC.).
 XX
 PI Tang Yr, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX
 DR WBI: 2001-476164/51.
 DR N-PSDB; AAH38760

XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 antibodies and research use.
 PS Claim 20; Page 1102-1103; 1275pp; English.

XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX
 SQ Sequence 384 AA;

Query Match 95.5%; Score 533; DB 4; Length 384;
 Best Local Similarity 95.4%; Pred. No. 1e-32; Mismatches 2; Indels 0; Gaps 0;
 Matches 103; Conservative 2; Standard: protein; 108 AA.

Qy 1 EIVLTQSGTGLSISPGERATLSCRASQSVSSSYLAWTQKPCQAPLLIVATSSRATGIP 60
 Db 167 EIVLTQSGTGLSISPGERATLSCRASQSVSSSYLAWTQKPCQAPLLIVGASSRATGIP 226

Qy 61 DRPSGSGSGSTDFTLTISRLPEDPAVYCCQXGSSPCSFQGQTCLEIK 108
 Db 227 DRPSGSGSGSTDFTLTISRLPEDPAVYCCQXGSSPCSFQGQTCLEIK 274

RESULT 1.4
 ADV4439 standard; protein; 108 AA.
 ID ADV4439
 XX
 AC ADV4439;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE PAX116 variable light chain variable region.
 XX
 KW anti-HIV; cytostatic; gene therapy; antibody engineering; diagnosis;
 KW HIV-infection; anti-HIV; chemotherapy; bone marrow transplantation;
 KW transplant rejection; prophylaxis; myeloproliferative disorder;

RESULT 1.3
 ADQ16703 standard; protein; 108 AA.
 ID ADQ16703

KW hematological disease; pax116.
 XX KW Antibody; phage display; protein therapy; antibody engineering;
 XX hemopoiesis; immunotherapy; Cardiant; Anorectic; Anorectic;
 KW cardiac failure; diabetes; obesity; light chain; tetanus toxoid; TPO;
 KW thrombopoietin.
 XX
 PN XX
 WO2004108078-A2.
 XX
 XX 16-DEC-2004.
 PD XX
 XX
 XX 26-MAY-2004; 2004WO-US016574.
 PR XX
 PR 02-JUN-2003; 2003US-00452590.
 XX
 PA (ALEX-') ALEXION PHARM INC.
 PA XX
 PI Bowdish KS, Frederickson S, Renshaw M, Orenicia C;
 XX DR
 DR 2005-031588/03.
 XX
 PT New immunoglobulin molecule comprising a region where amino acid residues
 PT corresponding to a portion of complementarity determining region (CDR) is
 PT replaced with a peptide mimetic, useful for treating, e.g. HIV-infected
 PT patients.
 XX
 PS Example 8; SEQ ID NO 123; 139pp; English.
 XX
 CC The invention describes an immunoglobulin molecule or its fragment
 CC comprising: a region where amino acid residues corresponding to at least
 CC a portion of two CDRs are replaced with a peptide mimetic selected from
 CC an EPO mimetic or TPO mimetic; or a region where amino acid residues
 CC corresponding to at least a portion of a CDR is replaced by a peptide
 CC mimetic including SEQ ID NO. 126 (not defined in the specification),
 CC where X at each occurrence represents any amino acid. Also described are:
 CC a nucleic acid encoding an immunoglobulin molecule or its fragment; an
 CC expression vector comprising the nucleic acid of (1); a host cell
 CC transformed with the expression vector of (2); producing an
 CC immunoglobulin molecule or its fragment; and a composition comprising the
 CC immunoglobulin or its fragment and a pharmaceutical carrier. Also
 CC described are: engineering immunoglobulin molecules or fragments;
 CC creation of a library of monoclonal antibodies; stimulating
 CC proliferation, differentiation, or growth of megakaryocytes; and
 CC activating a homodimeric receptor protein. The immunoglobulin molecules
 CC are useful for treating HIV-infected patients, patients undergoing
 CC chemotherapy, bone marrow transplant patients, stem cell transplant
 CC patients, or patients suffering from myeloproliferative disorders. This
 CC is the amino acid sequence of modified anti-tetanus toxoid antibody
 CC pax116 light chain variable region. The heavy chain of pax116 comprises
 CC two agonist TPO-mimetic peptides.
 XX
 SQ Sequence 108 AA;
 Query Match 95.3%; Score 532; DB 9; Length 108;
 Best Local Similarity 95.4%; Pred. No. 3.9e-33;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSSLAVYQKREGQAPRLIVATSSRATGIP 60
 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSSLAVYQKREGQAPRLIVATSSRATGIP 60
 Db 1 DRFGSGSGTGTDFLTISRLPEDFAVVQOQYGSSPCSPGQSTKLRIK 108
 Qy 61 DRFGSGSGTGTDFLTISRLPEDFAVVQOQYGSSPCSPGQSTKLRIK 108
 Db 61 DRFGSGSGTGTDFLTISRLPEDFAVVQOQYGSSPCSPGQSTKLRIK 108
 Qy 61 DRFGSGSGTGTDFLTISRLPEDFAVVQOQYGSSPCSPGQSTKLRIK 108
 Db 61 DRFGSGSGTGTDFLTISRLPEDFAVVQOQYGSSPCSPGQSTKLRIK 108
 RESULT 15
 AEB12911 AEB12911 standard; protein; 108 AA.
 ID AEB12911
 XX
 AC AEB12911;
 XX
 DT 08-SEP-2005 (first entry)
 XX Antibody paxB116 light chain variable region.

CC tetanus toxoid Fab antibody with grafted TPO mimetic peptides in place
CC of one or more of its CDRs.
XX

SQ Sequence 108 AA;

Query Match 95.3%; Score 532; DB 9; Length 108;
Best Local Similarity 95.4%; Pred. No. 3.9e-33;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EIVLTQSPTELISPGERATLSGRASQVSSYSLAWYQKPGQAPRLIYASSRATGIP 60
Db 1 EIVLTQSPTELISPGERATLSGRASQVSSYSLAWYQKPGQAPRLIYASSRATGIP 60
Qy 61 DRFGSGSGSTDFTLTISLEPEDFAVYTCQQYQSSSPCGFGQTKLTK 108
Db 61 DRFGSGSGSTDFTLTISLEPEDFAVYTCQQYQSSSPWTFGQGTVKELK 108

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OM protein - protein search, using sw model

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291.870 Million cell updates/sec

Title: US-10-041-860-49

Perfect score: 558

Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQQYQSSPCSFQGTKEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6_ptodata/1/iaa/5_COMBO.pep:*

2: /cgn2_6_ptodata/1/iaa/6_COMBO.pep:*

3: /cgn2_6_ptodata/1/iaa/H_COMBO.pep:*

4: /cgn2_6_ptodata/1/iaa/PCTUS_COMBO.pep:*

5: /cgn2_6_ptodata/1/iaa/RE_COMBO.pep:*

6: /cgn2_6_ptodata/1/iaa/backfile.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	530	95.0	108	1 US-08-232-081B-42	Sequence 42, App1
2	529	94.8	109	2 US-09-028-769B-16	Sequence 16, App1
3	529	94.8	109	2 US-09-490-070A-16	Sequence 16, App1
4	529	94.8	109	2 US-09-490-153-16	Sequence 16, App1
5	529	94.8	109	2 US-09-490-324-16	Sequence 16, App1
6	525	94.1	108	1 US-08-488-113B-150	Sequence 150, App1
7	525	94.1	108	1 US-08-477-484B-150	Sequence 150, App1
8	525	94.1	108	1 US-08-64-360-150	Sequence 150, App1
9	525	94.1	108	2 US-08-839-765-150	Sequence 150, App1
10	525	94.1	108	2 US-09-136-389-150	Sequence 150, App1
11	525	94.1	108	2 US-09-61-838-150	Sequence 150, App1
12	524	94.1	108	2 US-09-711-485-150	Sequence 150, App1
13	524	94.0	226	2 US-09-456-090A-50	Sequence 50, App1
14	524.5	94.0	226	2 US-09-45-090A-86	Sequence 86, App1
15	524.5	94.0	226	2 US-09-455-234-50	Sequence 50, App1
16	524.5	94.0	226	2 US-09-455-234-86	Sequence 86, App1
17	521	93.4	235	2 US-09-47-087-14	Sequence 14, App1
18	521	93.4	235	2 US-09-47-087-65	Sequence 65, App1
19	518.5	92.9	226	2 US-09-456-090A-80	Sequence 80, App1
20	518.5	92.9	226	2 US-09-45-234-80	Sequence 80, App1
21	518.5	92.8	236	2 US-09-853-34	Sequence 34, App1
22	518	92.8	108	2 US-09-241-274-178	Sequence 178, App1
23	518	92.8	108	2 US-09-84-798-178	Sequence 178, App1
24	512.5	92.0	236	2 US-09-855-053-38	Sequence 38, App1
25	512.5	91.8	226	2 US-09-456-090A-74	Sequence 74, App1
26	511.5	91.8	226	2 US-09-45-234-74	Sequence 74, App1
27	511.5	91.7	226	2 US-09-456-090A-42	Sequence 42, App1

ALIGMENTS

RESULT 1

US-08-232-081B-42

; Patent No. 5886152

; Sequence 42, Application US/08232081B

; GENERAL INFORMATION:

; APPLICANT: NAKATANI, TOMOYUKI

; APPLICANT: GOMI, HIDENYUKI

; APPLICANT: WIDENES, JOHN

; APPLICANT: NOGUCHI, HIROSHI

; TITLE OF INVENTION: HUMANIZED B-B10

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEES: BIRCH, STEWART, KOLASCH AND BIRCH

; STREET: PO BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 222040-0747

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232, 081B

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: SVENSSON, LEONARD R

REGISTRATION NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 20-3484

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-232-081B-42

Query Match 95.0%; Score 530; DB 1; Length 108;

Best Local Similarity 94.4%; Pred. No. 1.5e-42;

Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSRCAASQSVSSSYLANYQQKPGQAPRILIVATSSRATGIP 60

Db 1 EIVLTQSPGTLSLSPGERATLSRCAASQSVSSSYLANYQQKPGQAPRILIVATSSRATGIP 60

Qy 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPOSFGQGTKLRIK 108
 Db 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPOSFGQGTKLRIK 108

RESULT 2
 US-09-025-769B-16
 Sequence 16, Application US/09025769B
 Patent No. 6300064
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Ilag, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James P. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 INFORMATION FOR SEQ ID NO: 16:
 TELEFAX: (212) 596-9090
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acids
 TYPE: amino acid
 STRANDBIDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-025-769B-16

Query Match 94.8%; Score 529; DB 2; Length 109;
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;
 Matches 102; Conservative 3; Miatches 0; Indels 0; Gaps 0;

RESULT 4
 US-09-490-153-16
 Sequence 16, Application US/09490153
 Patent No. 6706484
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Ilag, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CURRENT APPLICATION DATA:
 ADDRESSEE: James P. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York

Qy 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPOSFGQGTKLRIK 108
 Db 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPOSFGQGTKLRIK 108
 RESULT 3
 US-09-490-070A-16
 Sequence 16, Application US/09490070A
 Patent No. 6636248
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Ilag, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CURRENT APPLICATION DATA:
 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
 STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,070A
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31,398
 REFERENCE/DOCKET NUMBER: 37629-00055
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acids
 TYPE: amino acid
 STRANDBIDNESS: <unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-490-070A-16

Query Match 94.8%; Score 529; DB 2; Length 109;
 Best Local Similarity 94.4%; Pred. No. 1.8e-42;
 Matches 102; Conservative 3; Miatches 3; Indels 0; Gaps 0;
 Qy 1 BIVLTQSPGTLSLSPERATLSRASQVSQSYLAWYQKPGQAPLLIYATSSRATGIP 60
 Db 1 BIVLTQSPGTLSLSPERATLSRASQVSQSYLAWYQKPGQAPLLIYASSRATGIP 60
 Qy 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPOSFGQGTKLRIK 108
 Db 61 DRFGSGSGTDTFLTISRLPEDPAVYCCQYGSPOSFGQGTKLRIK 108

COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION NUMBER: US/09/490,153
 FILING DATE: 24-Jan-2000
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)536-9030
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acid(s)
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-490-153-16

	Query Match	Score 94.8%;	DB 2;	Length 109;
Qy	Best Local Similarity 94.4%;	Pred. No. 1.8e-42;		
Db	Matches 102;	Mismatches 3;	Indels 0	
Qy	1 BIVLTSQPGTISLSPGERATLSCRASQSVSSSYLAWYQQXPQGPQLRLIYAT			
Db	1 BIVLTSQPGTISLSPGERATLSCRASQSVSSSYLAWYQQXPQGPQLRLIYGA			
Qy	61 DRFGSGSGTIDFTLTLISRLRBDPAVYCCQYGGSSPCSFQGTKLBIK 108			
Db	61 DRFGSGSGTIDFTLTLISRLRBDPAVYCCQYGGSSPCSFQGTKLBIK 108			

RESULT 5
 US-09-490-324-16
 Sequence 16, Application US/09490324
 Patent No. 6828422
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Limming
 Moroney, Simon
 Plueckthun, Andreas
 TITLE OF INVENTION: Protein (Poly) peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neauvin
 STREET: 1231 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,324
 FILING DATE: 24-Jan-2000

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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 596-9000
TELEPHONE: (212) 596-9090

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-324-16

Query Match 94.8%; Score 529; DB 2; Length 109;
Best Local Similarity 94.4%; Pred. No. 1.8e-42; 3. Missmatches 3; Indels 0; Gaps 0
Matches 102; Conservative 102;
GENERAL INFORMATION:
APPLICANT: Carroll, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

RESULT 6
US-08-438-113B-150
Sequence 150, Application US/08488113B
; Patient No. 5744380
; GENERAL INFORMATION:
; APPLICANT: Carroll, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707

```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US07/200-70, P3.C2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEX: 312/707-9155
 TELEFAX: 312/707-9148
 INFORMATION FOR SEQ ID NO: 150:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: amino acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-488-113B-150

Query Match 94.1%; Score 525; DB 1; Length 108;
 Best Local Similarity 94.4%; Pred. No. 4.3e-42;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCASQSSVSSYLAQKPGQAAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCASQSSVSSYLAQKPGQAAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDEFTLTISRLPEDFATYCCQYGSSPSFQGSKTLEIK 108
 Db 61 DRFGSGSGTDEFTLTISRLPEDFATYCCQYGSSEXTFGQGSKVIEIK 108

RESULT 7
 US-08-477-484B-150
 Sequence 150, Application US/08477484B
 Patent No. 5756699
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 169
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,484B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707

RESULT 8
 US-08-477-484B-150
 Sequence 150, Application US/08646360
 Patent No. 5837491
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707

APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE DOCKET NUMBER: 11022US09/200-70.P3.C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 150:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: amino acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-646-360-150

Query Match 94.1%; Score 525; DB 1; Length 108;
 Best Local Similarity 94.1%; Pred. No. 4.3e-12; Indels 0; Gaps 0;
 Matches 102; Conservative 2; Mismatches 4; Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIVLTQSGTTLSPGERATLSCASQVSQSSYLAIVQKPGQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSGTTLSPGERATLSCASQVSQSSYLAIVQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDTFLTISRLSLEPDAVYCCQYGSPPCSFGQCTKLEIK 108
 Db 61 DRFGSGSGTDTFLTISRLSLEPDAVYCCQYGSPPCSFGQCTKVEIK 108

RESULT 9
 US-08-839-765-150
 Sequence 150, Application US/08839765
 Patent No. 6146631
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 ATTORNEY: Carroll, Stephen F.
 APPLICANT: Studnica, Gary M.
 APPLICANT: Studnica, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 169
 NUMBER OF SEQUENCES: 169
 CURRENT APPLICATION DATA:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/839,765
 FILING DATE: 15-APR-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567

RESULT 10
 US-09-136-389-150
 Sequence 150, Application US/09136389
 Patent No. 6146850
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 ATTORNEY: Carroll, Stephen F.
 APPLICANT: Studnica, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 1173
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,389
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/646,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567

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; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE B TYPE: protein
; US-09-136-389-150

Query Match Score 94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.3e-42; Indels 0; Gaps 0;
Matches 102; Conservative 2; Mismatches 4; DB 0-9-610-838-150

RESULT 12
US-09-711-485-150
; Sequence 150, Application US/09711485
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnitska, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707

; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70-P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-150

Query Match Score 94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.3e-42; Indels 4; Gaps 0;
Matches 102; Conservative 2; Mismatches 4; DB 0-9-610-838-150

Query Match Score 94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.3e-42; Indels 0; Gaps 0;
Matches 102; Conservative 2; Mismatches 4; DB 0-9-610-838-150

; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnitska, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
;
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; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA: US 07/187,567
 ; FILING DATE: 04-NOV-1991.
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REREFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; FAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Protein
 ; US-09-711-485-150

Query Match 94.1% Score 525; DB 2; Length 108;
 Best Local Similarity 94.4%; Pred. No. 4.3e-42; Indels 0; Gaps 0;
 Matches 102; Conservative 2; Mismatches 4;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSSYLAQKPCQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSSYLAQKPCQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDFLTISRLSPEDFAYVYCOQYCGSSPPYTFQGTKLK 108
 Db 61 DRFGSGSGTDFLTISRLSPEDFAYVYCOQYCGSSPPYTFQGTKLK 108

RESULT 13

US-09-456-090A-50
 ; Sequence 50, Application US/09456090A
 ; Patent No. 6680209
 ; GENERAL INFORMATION:
 ; APPLICANT: Buechler, Joe
 ; APPLICANT: Valkirs, Gunars
 ; APPLICANT: Gray, Jeff
 ; APPLICANT: Lonberg, Niils
 ; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
 ; FILE REFERENCE: 020015-000200US
 ; CURRENT APPLICATION NUMBER: US/09/456,090A
 ; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 50
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: MI-23L
 ; US-09-456-090A-50

Query Match 94.0% Score 524.5; DB 2; Length 226;
 Best Local Similarity 95.4%; Pred. No. 1.1e-41; Indels 1; Gaps 1;
 Matches 104; Conservative 1; Mismatches 3;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSSYLAQKPCQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSSYLAQKPCQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTDFLTISRLSPEDFAYVYCOQYCGSS-PCSPFGQGTKLK 108
 Db 61 DRFGSGSGTDFLTISRLSPEDFAYVYCOQYCGSSPPYTFQGTKLK 108

RESULT 14

US-09-456-090A-86
 ; Sequence 86, Application US/09456090A
 ; Patent No. 6680209

Search completed: May 15, 2006, 17:06:01
 Job time : 31.5923 secs

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Result No.	Score	Query	Match	Length	DB ID	Description
1	558	100.0	108	4	US-10-041-860-49	Sequence 49, App1
2	558	100.0	108	4	US-10-041-860-225	Sequence 225, App1
3	558	100.0	108	4	US-10-041-860-259	Sequence 259, App1
4	558	100.0	108	4	US-10-041-860-375	Sequence 375, App1
5	558	100.0	108	4	US-10-065-383-4	Sequence 4, App1
6	535	95.9	108	5	US-10-891-659-84	Sequence 84, App1
7	535	95.9	108	5	US-10-891-659-131	Sequence 131, App1
8	533	95.9	128	5	US-10-910-901-18	Sequence 18, App1
9	533	95.5	108	4	US-10-109-762-156	Sequence 156, App1
10	533	95.5	130	4	US-10-693-629-46	Sequence 46, App1
11	532	95.3	108	4	US-10-307-724-123	Sequence 123, App1
12	532	95.3	108	5	US-10-737-290-123	Sequence 123, App1
13	532	95.3	109	5	US-10-725-962-27	Sequence 27, App1
14	532	95.3	120	5	US-10-506-743-2	Sequence 2, App1
15	532	95.3	130	5	US-10-737-290-161	Sequence 161, App1
16	532	95.3	215	4	US-10-307-724-122	Sequence 122, App1
17	532	95.3	215	5	US-10-737-290-122	Sequence 122, App1
18	532	95.3	239	5	US-10-737-290-142	Sequence 142, App1
19	530	95.0	384	4	US-10-291-265-804	Sequence 804, App1
20	530	95.0	384	4	US-10-291-265-805	Sequence 805, App1
21	530	95.0	384	4	US-10-291-265-806	Sequence 806, App1
22	530	95.0	384	4	US-10-291-265-807	Sequence 807, App1
23	529	94.8	108	4	US-10-289-711-21	Sequence 21, App1
24	529	94.8	108	4	US-10-584-109-21	Sequence 21, App1
25	528	94.6	108	3	US-09-948-939-9	Sequence 9, App1
26	528	94.6	108	6	US-11-040-846-9	Sequence 9, App1
27	526	94.3	108	4	US-10-338-366-4	Sequence 4, App1

APPLICANT: Weber, Richard
 APPLICANT: Bezabeh, Binyam
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: AGENIX.051A
 CURRENT APPLICATION NUMBER: US/10/041,860
 CURRENT FILING DATE: 2002-01-07
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 225
 LENGTH: 108
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-225

Query Match 100.0%; Score 558; DB 4; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.5e-40;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIATSSRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLPEPDFAVYYCQQYGGSPCSFGQGTKLRIK 108
 Db 61 DRFGSGSGTDFTLTISRLPEPDFAVYYCQQYGGSPCSFGQGTKLRIK 108

RESULT 3
 US-10-041-860-259
 Sequence 259, Application US/10041860
 Publication No. US20030157109A1

GENERAL INFORMATION:
 APPLICANT: Corvalan, Jose R.F.
 APPLICANT: Jia, Xiao-Chi
 APPLICANT: Feng, Xiao
 APPLICANT: Yang, Xiao-Dong
 APPLICANT: Chen, Francine
 APPLICANT: Gazit, Gadi
 APPLICANT: Weber, Richard
 APPLICANT: Bezabeh, Binyam
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES
 FILE REFERENCE: AGENIX.051A
 CURRENT APPLICATION NUMBER: US/10/041,860
 CURRENT FILING DATE: 2002-01-07
 NUMBER OF SEQ ID NOS: 377
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 259
 LENGTH: 108
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-041-860-259

Query Match 100.0%; Score 558; DB 4; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.5e-40;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIATSSRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLPEPDFAVYYCQQYGGSPCSFGQGTKLRIK 108
 Db 61 DRFGSGSGTDFTLTISRLPEPDFAVYYCQQYGGSPCSFGQGTKLRIK 108

RESULT 4
 US-10-041-860-375
 Sequence 375, Application US/10041860
 Publication No. US20030157109A1

GENERAL INFORMATION:
 APPLICANT: Corvalan, Jose R.F.

RESULT 5
 US-10-665-383-4
 Sequence 4, Application US/10665383
 Publication No. US20040141969A1

GENERAL INFORMATION:
 APPLICANT: Floee, Juergen
 APPLICANT: Gazit, Gadi
 APPLICANT: Keyt, Bruce
 APPLICANT: LaRochelle, William
 APPLICANT: Lichtenstein, Henri
 TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
 FILE REFERENCE: AGENIX.052A
 CURRENT APPLICATION NUMBER: US/10/665,383
 CURRENT FILING DATE: 2003-09-16
 PRIOR APPLICATION NUMBER: 60/411,137
 PRIOR FILING DATE: 2002-09-16
 NUMBER OF SEQ ID NOS: 97
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 108
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-665-383-4

Query Match 100.0%; Score 558; DB 4; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.5e-40;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIATSSRATGIP 60

Qy 61 DRFGSGSGTDFTLTISRLPEPDFAVYYCQQYGGSPCSFGQGTKLRIK 108
 Db 61 DRFGSGSGTDFTLTISRLPEPDFAVYYCQQYGGSPCSFGQGTKLRIK 108

RESULT 6
 US-10-891-658-84

GENERAL INFORMATION:
 APPLICANT: Corvalan, Jose R.F.

```

; Sequence 84, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; PRIORITY FILING DATE: 2004-07-15
; PRIORITY APPLICATION NUMBER: US 60/487,431
; PRIORITY FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 84
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapien
us-10-891-658-84

Db      61 DRFGSGSGSGTDFLTISRLPEDPDFAVYYCQQGSSPYPFGQGTLEIK 108
; RESULT 8
; US-10-910-901-18
; Sequence 18, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO c-NET
; FILE REFERENCE: ABX-PFS
; CURRENT APPLICATION NUMBER: US/10/910,901
; PRIORITY FILING DATE: 2004-08-03
; PRIORITY APPLICATION NUMBER: US 60/492,432
; PRIORITY FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO: 18
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-18

Query Match      95.9%;  Score 535;  DB 5;  Length 128;
Best Local Similarity  96.3%;  Pred. No. 4.1e-38;
Matches 104;  Conservative 1;  Mismatches 3;  Indels 0;  Gaps 0;
Qy      1 EIVLTOQSPGTLSLSPGERATLSCRASQVSSEYIAYQKPGQAPRLIYATSSRATGIP 60
Db      1 EIVLTOQSPGTLSLSPGERATLSCRASQVSSEYIAYQKPGQAPRLIYATSSRATGIP 60
Qy      61 DRFGSGSGSGTDFLTISRLPEDPDFAVYYCQQGSSPYPFGQGTLEIK 108
Db      61 DRFGSGSGSGTDFLTISRLPEDPDFAVYYCQQGSSPYPFGQGTLEIK 108
; RESULT 9
; US-10-309-762-156
; Sequence 156, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIORITY FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 156
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-156

Query Match      95.5%;  Score 533;  DB 4;  Length 108;
Best Local Similarity  95.4%;  Pred. No. 6.1e-38;
Matches 103;  Conservative 2;  Mismatches 3;  Indels 0;  Gaps 0;
Qy      1 EIVLTOQSPGTLSLSPGERATLSCRASQVSSEYIAYQKPGQAPRLIYATSSRATGIP 60
Db      1 EIVLTOQSPGTLSLSPGERATLSCRASQVSSEYIAYQKPGQAPRLIYATSSRATGIP 60
Qy      61 DRFGSGSGSGTDFLTISRLPEDPDFAVYYCQQGSSPYPFGQGTLEIK 108
Db      61 DRFGSGSGSGTDFLTISRLPEDPDFAVYYCQQGSSPYPFGQGTLEIK 108
; RESULT 7
; US-10-891-658-131
; Sequence 131, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; PRIORITY FILING DATE: 2004-07-15
; PRIORITY APPLICATION NUMBER: US 60/487,431
; PRIORITY FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 131
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapien
us-10-891-658-131

Query Match      95.9%;  Score 535;  DB 5;  Length 108;
Best Local Similarity  96.3%;  Pred. No. 4.1e-38;
Matches 104;  Conservative 1;  Mismatches 3;  Indels 0;  Gaps 0;
Qy      1 EIVLTOQSPGTLSLSPGERATLSCRASQVSSEYIAYQKPGQAPRLIYATSSRATGIP 60
Db      1 EIVLTOQSPGTLSLSPGERATLSCRASQVSSEYIAYQKPGQAPRLIYATSSRATGIP 60
Qy      61 DRFGSGSGSGTDFLTISRLPEDPDFAVYYCQQGSSPYPFGQGTLEIK 108

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RESULT 10
 US-10-693-629-46
 Sequence 4.6, Application US/10693629
 Publication No. US20040120948A1
 GENERAL INFORMATION:
 APPLICANT: KIRIN BEER KABUSHIKI KAISHA
 APPLICANT: MIKAYAMA, Toshihumi
 APPLICANT: YOSHIDA, Hitoshi
 APPLICANT: FORCE, Walker, R.
 APPLICANT: CHEN, Xinsjie
 APPLICANT: TAKAHASHI, Nobuaki
 TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
 FILE REFERENCE: 021286-0306473
 CURRENT APPLICATION NUMBER: US/10/693, 629
 CURRENT FILING DATE: 2003-11-13
 PRIOR APPLICATION NUMBER: PCT/US01/13672
 PRIOR FILING DATE: 2001-04-27
 PRIOR APPLICATION NUMBER: US/09/844, 684
 PRIOR APPLICATION NUMBER: JP2001/142482
 PRIOR FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: JP2001/310535
 PRIOR FILING DATE: 2001-04-27
 PRIOR APPLICATION NUMBER: US/10/040, 244
 PRIOR FILING DATE: 2001-10-05
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 46
 LENGTH: 130
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-693-629-46

Query Match 95.5%; Score 533; DB 4; Length 130;
 Best Local Similarity 95.4%; Pred. No. 7.3e-38;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLISLSPGERATLSCRASOSVSSYLAQKPGQAPRLIYATSSRATGIP 60
 Db 21 EIVLTQSPGTLISLSPGERATLSCRASOSVSSYLAQKPGQAPRLIYATSSRATGIP 80

Qy 61 DRFGSGSGSGTDPFLTISRLPEDFAYYCCQYGSSSPCSFGQTKLEIK 108
 Db 81 DRFGSGSGSGTDPFLTISRLPEDFAYYCCQYGSSPFTFGQTRLEIK 128

RESULT 11
 US-10-307-724-123
 Sequence 1.23, Application US/10307724
 Publication No. US2003032972A1
 GENERAL INFORMATION:
 APPLICANT: Bowdish, Katherine S.
 APPLICANT: Frederickson, Shana
 APPLICANT: Renshaw, Mark
 TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
 FILE REFERENCE: 1087-261P
 CURRENT APPLICATION NUMBER: US/10/307,724
 CURRENT FILING DATE: 2002-12-02
 PRIOR APPLICATION NUMBER: US 10/006,593
 PRIOR FILING DATE: 2001-12-05
 PRIOR APPLICATION NUMBER: US 10/452,590
 PRIOR FILING DATE: 2003-06-02
 PRIOR APPLICATION NUMBER: US 10/307,724
 PRIOR FILING DATE: 2002-12-02
 PRIOR APPLICATION NUMBER: US 10/006,593
 PRIOR FILING DATE: 2001-12-05
 PRIOR APPLICATION NUMBER: US 60/251,448
 PRIOR FILING DATE: 2000-12-05
 PRIOR APPLICATION NUMBER: US 60/288,889
 PRIOR FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: US 60/294,068
 PRIOR FILING DATE: 2001-05-29
 NUMBER OF SEQ ID NOS: 193
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 123
 LENGTH: 108
 TYPE: PRT
 ORGANISM: artificial sequence
 FEATURE:

RESULT 12
 US-10-737-290-123
 Sequence 1.23, Application US/10737290
 Publication No. US2004025342A1
 GENERAL INFORMATION:
 APPLICANT: Bowdish, Katherine S.
 APPLICANT: Frederickson, Shana
 APPLICANT: Renshaw, Mark
 APPLICANT: Orcencia, Cecilia
 TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
 FILE REFERENCE: 1087-2 CIP III
 CURRENT APPLICATION NUMBER: US/10/737,290
 CURRENT FILING DATE: 2003-12-15
 PRIOR APPLICATION NUMBER: US 10/452,590
 PRIOR FILING DATE: 2003-06-02
 PRIOR APPLICATION NUMBER: US 10/307,724
 PRIOR FILING DATE: 2002-12-02
 PRIOR APPLICATION NUMBER: US 10/006,593
 PRIOR FILING DATE: 2001-12-05
 PRIOR APPLICATION NUMBER: US 60/251,448
 PRIOR FILING DATE: 2000-12-05
 PRIOR APPLICATION NUMBER: US 60/288,889
 PRIOR FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: US 60/294,068
 PRIOR FILING DATE: 2001-05-29
 NUMBER OF SEQ ID NOS: 193
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 123
 LENGTH: 108
 TYPE: PRT
 ORGANISM: artificial sequence
 FEATURE:

RESULT 13
 US-10-725-962-27
 Sequence 2.7, Application US/10725962
 Publication No. US20050013809A1
 GENERAL INFORMATION:
 APPLICANT: Samuel M. Owens
 APPLICANT: Frank I. Carroll
 APPLICANT: Phillip Abraham
 APPLICANT: Melinda G. Gunnell

APPLICANT: Mary Haak-Frendschoo
 APPLICANT: Xiao Peng
 TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE

FILE REFERENCE: ABSENIX_071A
 CURRENT APPLICATION NUMBER: US/10/725, 562
 CURRENT FILING DATE: 2003-12-02
 PRIOR APPLICATION NUMBER: 60/430717
 PRIOR FILING DATE: 2002-12-02
 NUMBER OF SEQ ID NOS: 141
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 27
 LENGTH: 109
 TYPE: PRT
 ORGANISM: *Mus musculus*
 US-10-725-942-27

Query Match 95.3%; Score 532; DB 5; Length 109;
 Best Local Similarity 95.4%; Pred. No. 7.4e-38;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSGTLSLSPGERATLSCRASQVSQSSYLAWYQKPCQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSGTLSLSPGERATLSCRASQVSQSSYLAWYQKPCQAPRLIYATSSRATGIP 60

RESUL 14
 US-10-506-743-2
 ; Sequence 2, Application US/10506743
 ; Publication No. US2005010614041
 ; GENERAL INFORMATION
 ; APPLICANT: Lancaster, Joanne Sloan
 ; TITLE OF INVENTION: Antagonistic Anti-hFas Ligand Human Antibodies and Fragments
 ; TITLE OF INVENTION: Thereof
 ; FILE REFERENCE: X15450 - National Stage
 ; CURRENT APPLICATION NUMBER: US/10/506,743
 ; CURRENT FILING DATE: 2004-09-03
 ; PRIOR APPLICATION NUMBER: 60/367,054
 ; PRIOR FILING DATE: 2002-03-21
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 2
 ; TYPE: PRT
 ; ORGANISM: *Homo sapiens*
 US-10-506-743-2

Query Match 95.3%; Score 532; DB 5; Length 120;
 Best Local Similarity 95.4%; Pred. No. 8.2e-38;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSGTLSLSPGERATLSCRASQVSQSSYLAWYQKPCQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSGTLSLSPGERATLSCRASQVSQSSYLAWYQKPCQAPRLIYATSSRATGIP 60

RESUL 15
 US-10-737-290-161
 ; Sequence 161, Application US/10737290
 ; PUBLICATION NO. US20040253242A1
 ; GENERAL INFORMATION
 ; APPLICANT: Bowdish, Katherine S.
 ; APPLICANT: Frederickson, Shana
 ; APPLICANT: Renshaw, Mark
 ; APPLICANT: Orencia, Cecilia
 ; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES

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GenCore version 5.1.8

OM protein - protein search, using sw model.

Run on: May 15, 2006, 17:21:22 ; Search time 17.1502 Seconds

(without alignments)
295.651 Million cell updates/sec

Title: US-10-041-860-49

Perfect score: 558

Sequence: 1 EIVITQSPTLISLSPGERAT.....CQQYGSFCSPCSFGQGTKLBIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries
Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Database : Published Applications AA_New:
1: /SIDSS5/ptodata/1/pubpa/US06_NEW_PUB.PEP1: *
2: /SIDSS5/ptodata/1/pubpa/US06_NEW_PUB.PEP1: *
3: /SIDSS5/ptodata/1/pubpa/US07_NEW_PUB.PEP1: *
4: /SIDSS5/ptodata/1/pubpa/US08_NEW_PUB.PEP1: *
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6: /SIDSS5/ptodata/1/pubpa/US09_NEW_PUB.PEP1: *
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10: /SIDSS5/ptodata/1/pubpa/US10_NEW_PUB.PEP1: *
11: /SIDSS5/ptodata/1/pubpa/US11_NEW_PUB.PEP1: *
12: /SIDSS5/ptodata/1/pubpa/US60_NEW_PUB.PEP1: *

RESULT 1

US-11-000-463-804

; Sequence 804, Application US/11000463
; Publication No. US2005266123A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong B.
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radivoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 75CIPACN

CURRENT APPLICATION NUMBER: US/11/000,463

CURRENT FILING DATE: 2004-11-29

PRIOR APPLICATION NUMBER: 10/291,265

PRIOR FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: PCT/US01/02623

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 09/922,279

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: 09/617,746

PRIOR FILING DATE: 2000-07-17

PRIOR APPLICATION NUMBER: 09/631,451

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 09/633,870

PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 944

SOFTWARE: FastSEQ for Windows Version 3.0

SBQ ID NO 804

LENGTH: 384

TYPE: PRT

ORGANISM: Homo sapiens

US-11-000-463-804

Result No.	Score	Query	Match	Length	DB ID	Description
1	530	95.0	384	11	US-11-000-463-804	Sequence 804, App
2	530	95.0	384	11	US-11-000-463-805	Sequence 805, App
3	530	95.0	384	11	US-11-000-463-806	Sequence 806, App
4	529	94.8	109	9	US-10-834-397-16	Sequence 16, App1
5	528	94.6	247	11	US-11-056-925-8	Sequence 8, App1
6	528	94.6	249	11	US-11-056-925-4	Sequence 4, App1
7	526	94.3	108	9	US-10-850-635-6	Sequence 6, App1
8	521	94.2	131	9	US-10-721-733-27	Sequence 27, App1
9	524	93.9	108	9	US-10-850-635-4	Sequence 4, App1
10	520	93.9	108	11	US-11-051-533-58	Sequence 58, App1
11	524	93.9	128	11	US-11-051-533-60	Sequence 60, App1
12	523	93.7	108	10	US-11-211-917-113	Sequence 113, App1
13	521	93.4	235	11	US-11-128-900-14	Sequence 14, App1
14	521	93.4	235	11	US-11-128-900-65	Sequence 65, App1
15	520	93.2	108	9	US-10-982-440-32	Sequence 32, App1
16	520	93.2	108	9	US-10-982-440-36	Sequence 36, App1
17	518	92.8	108	10	US-11-064-174-178	Sequence 178, App
18	514.5	92.2	113	11	US-11-049-536-104	Sequence 104, App
19	514.5	92.2	113	11	US-11-199-739-104	Sequence 31, App1
20	513	91.9	291	11	US-11-041-095-60	Sequence 32, App1

Query Match Score 530; DB 11; Pred. No. 8.5e-37; Length 384;
Best Local Similarity 94.4%;

RESULT 2
US-11-000-463-805
Sequence 805, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radivoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIPACN
CURRENT APPLICATION NUMBER: US/11/000, 463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291, 265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/922, 279
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491, 404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617, 746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631, 451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633, 870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 806
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-11-000-463-806

Query Match 95.0%; Score 530; DB 11; Length 384;
Best Local Similarity 94.4%; Pred. No. 8.5e-37;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Matches 102; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSRASQSSSYLAWQQKPGQAPRLLIYATSSRATGIP 60
Db 170 EIVLTQSPGTLSLSPGERATLSRASQSSSYLAWQQKPGQAPRLLIYATSSRATGIP 229

Qy 61 DRFGSGSGTDFLTISLEPEDFAVYQQYQQSSPCSFQGQTKLEIK 108
Db 230 DRFGSGSGTDFLTISLEPEDFAVYQQYQQSSPCSFQGQTKVDIK 277

RESULT 4
US-11-000-463-807
Sequence 807, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radivoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIPACN
CURRENT APPLICATION NUMBER: US/11/000, 463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291, 265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 001-01-25
PRIOR APPLICATION NUMBER: 09/922, 279
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491, 404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617, 746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631, 451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633, 870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 805
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-11-000-463-805

Query Match 95.0%; Score 530; DB 11; Length 384;
Best Local Similarity 94.4%; Pred. No. 8.5e-37;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Matches 102; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSRASQSSSYLAWQQKPGQAPRLLIYATSSRATGIP 60
Db 170 EIVLTQSPGTLSLSPGERATLSRASQSSSYLAWQQKPGQAPRLLIYATSSRATGIP 229

Qy 61 DRFGSGSGTDFLTISLEPEDFAVYQQYQQSSPCSFQGQTKLEIK 108
Db 230 DRFGSGSGTDFLTISLEPEDFAVYQQYQQSSPCSFQGQTKVDIK 277

RESULT 3
US-11-000-463-806
Sequence 806, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radivoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIPACN
CURRENT APPLICATION NUMBER: US/11/000, 463
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291, 265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 001-01-25
PRIOR APPLICATION NUMBER: 09/922, 279
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491, 404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617, 746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631, 451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633, 870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 805
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
US-11-000-463-805

Query Match 95.0%; Score 530; DB 11; Length 384;
Best Local Similarity 94.4%; Pred. No. 8.5e-37;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Matches 102; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSRASQSSSYLAWQQKPGQAPRLLIYATSSRATGIP 60
Db 170 EIVLTQSPGTLSLSPGERATLSRASQSSSYLAWQQKPGQAPRLLIYATSSRATGIP 229

Qy 61 DRFGSGSGTDFLTISLEPEDFAVYQQYQQSSPCSFQGQTKLEIK 108
Db 230 DRFGSGSGTDFLTISLEPEDFAVYQQYQQSSPCSFQGQTKVDIK 277

PRIOR FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: 09/491,404
 PRIOR FILING DATE: 2000-01-25
 PRIOR APPLICATION NUMBER: 09/617,746
 PRIOR FILING DATE: 2000-07-17
 PRIOR APPLICATION NUMBER: 09/631,451
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: 09/633,870
 PRIOR FILING DATE: 2000-09-15
 NUMBER OF SEQ ID NOS: 944
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 807
 LENGTH: 384
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-000-463-807

Query Match 95.0%; Score 530; DB 11; Length 384;
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSIPLSPGERATLSRASQVSSTYLAQKPGQAPRLIYATSSRATGIP 60
 Db 170 EIVLTQSPGTLSIPLSPGERATLSRASQVSSTYLAQKPGQAPRLIYATSSRATGIP 229

Query Match 95.0%; Score 530; DB 11; Length 384;
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 61 DRFGSGSGTGTDFLTISLEPEDFAYVYCQYGSPTFGQSTKVDIK 108
 Db 230 DRFGSGSGTGTDFLTISLEPEDFAYVYCQYGSPTFGQSTKVDIK 277

RESULT 5
 ; Sequence 16, Application US/10834397
 ; Publication No. US20060003334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; Pack, Peter
 ; Ilag, Vic
 ; Ge, Liming
 ; Moroney, Simon
 ; Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein (Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; ZIP: 10021
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/834,397
 ; FILING DATE: 29-Apr-2004
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/490,324
 ; FILING DATE: 24-Jan-2000
 ; APPLICATION NUMBER: US/09/025,769
 ; FILING DATE: 18-Feb-1998
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: James F. Haley, Jr., Esq.
 ; REGISTRATION NUMBER: 27,704
 ; PRIORITY/DOCKET NUMBER: MORPHO/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)596-9000
 ; TELEFAX: (212)596-9090
 ; INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-10-834-397-16

Query Match 94.8%; Score 529; DB 9; Length 109;
 Best Local Similarity 94.4%; Pred. No. 3.4e-37;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSIPLSPGERATLSRASQVSSTYLAQKPGQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSIPLSPGERATLSRASQVSSTYLAQKPGQAPRLIYATSSRATGIP 60

RESULT 6
 ; Sequence 8, Application US/11056825
 ; Publication No. US20050255109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Felding-Habermann, Brunhilde
 ; APPLICANT: Janda, Kim D.
 ; APPLICANT: Saven, Alan
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
 ; FILE REFERENCE: SCRP-0042
 ; CURRENT APPLICATION NUMBER: US/11/056,825
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: US 60/626,726
 ; PRIOR FILING DATE: 2004-11-10
 ; PRIOR APPLICATION NUMBER: US 60/544,807
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO: 8
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 ; US-11-056-825-8

Query Match 94.6%; Score 528; DB 11; Length 247;
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSIPLSPGERATLSRASQVSSTYLAQKPGQAPRLIYATSSRATGIP 60
 Db 127 EIVLTQSPGTLSIPLSPGERATLSRASQVSSTYLAQKPGQAPRLIYATSSRATGIP 186

Query Match 94.6%; Score 528; DB 11; Length 247;
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 61 DRFGSGSGTGTDFLTISLEPEDFAYVYCQYGSPTFGQSTKVDIK 108
 Db 187 DRFGSGSGTGTDFLTISLEPEDFAYVYCQYGSPTFGQSTKVDIK 234

RESULT 7
 ; Sequence 4, Application US/11056825
 ; Publication No. US20050255109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Felding-Habermann, Brunhilde
 ; APPLICANT: Janda, Kim D.
 ; APPLICANT: Saven, Alan
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
 ; FILE REFERENCE: SCRP-0042
 ; CURRENT APPLICATION NUMBER: US/11/056,825
 ; CURRENT FILING DATE: 2005-02-11

FILE REFERENCE: PH-1573-PCT
 CURRENT APPLICATION NUMBER: US/10/721,763
 CURRENT FILING DATE: 2003-11-26
 PRIORITY NUMBER: JP2001-150213
 PRIORITY NUMBER: JP2001-05-18
 PRIORITY NUMBER: JP2001-243040
 PRIORITY NUMBER: JP2001-08-09
 PRIORITY NUMBER: JP2001-314489
 PRIORITY NUMBER: JP2001-0-11
 NUMBER OF SEQ ID NOS: 45
 SEQ ID NO: 4
 LENGTH: 249
 TYPE: PRT
 ORGANISM: Artificial
 OTHER INFORMATION: Synthetic Construct
 US-11-056-825-4

Query Match 94.6%; Score 528; DB 11; Length 249;
 Best Local Similarity 94.4%; Pred. No. 8.5e-37;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60
 Db 127 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 186

Qy 61 DRFGSGSGTGTDEFTLTLISRLPEPDFAVYCCOYGSSPCFSQGTTKLEIK 108
 Db 187 DRFGSGSGTGTDEFTLTLISRLPEPDFAVYCCOYGSSEPFQQGTVDIK 234

RESULT 8
 US-10-850-635-6

Sequence 6, Application US/10850635
 Publication No. US20050287149A1
 GENERAL INFORMATION:
 APPLICANT: Keler, Tibor
 APPLICANT: Lowy, Israel
 APPLICANT: Vitale, Laura
 APPLICANT: Blanet, Diane
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST
 TITLE OF INVENTION: BACILLUS ANTHRACIS PROTECTIVE ANTIGEN
 FILE REFERENCE: MXI-305
 CURRENT APPLICATION NUMBER: US/10/850,635
 CURRENT FILING DATE: 2004-05-21
 PRIOR APPLICATION NUMBER: 60/472636
 PRIOR FILING DATE: 2003-05-21
 PRIOR APPLICATION NUMBER: 60/512336
 PRIOR FILING DATE: 2003-10-16
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 108
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-850-635-6

Query Match 94.3%; Score 526; DB 9; Length 108;
 Best Local Similarity 95.4%; Pred. No. 6e-37; Indels 4; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGTGTDEFTLTLISRLPEPDFAVYCCOYGSSPCFSQGTTKLEIK 108
 Db 61 DRFGSGSGTGTDEFTLTLISRLPEPDFAVYCCOYGSSEPFQQGTVDIK 108

RESULT 9
 US-10-721-763-27

Sequence 27, Application US/10721763
 Publication No. US20050249729A1
 GENERAL INFORMATION:
 APPLICANT: KIRIN BEER KABUSHIKI KAISHA
 TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY

RESULT 11
 US-11-051-453-58
 Sequence 58, Application US/11051453
 Publication No. US20050287150A1

```

; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESSA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN

; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MJU-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIORITY NUMBER: 60/542,357
; PRIORITY FILING DATE: 2004-02-06
; PRIORITY APPLICATION NUMBER: 60/613,854
; PRIORITY FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 58
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-58

Query Match . . . . . Score 524; DB 11; Length 108;
Best Local Similarity 93.9%; Pred. No. 9.8e-37;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0

Qy      1 DFIIVLTSQPGTLISLSPGERATLSCRASQSYSSSYLAWQKPGQAPRLLIYATSSRATGIP
Db      1 DFIIVLTSQPGTLISLSPGERATLSCRASQSYSSSYLAWQKPGQAPRLLIYAGASSRATGIP

Qy      61 DRFSSGGSGTDTFLTISRLSPEDFAVVYQQGSSPCSFQGTTLBIK 108
Db      61 DRFSSGGSGTDTFLTISRLSPEDFAVVYQQGSSSTWTFGQGTRVKEIK 108

; RESULT 12
US-11-051-453-60
; Sequence 60, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESSA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN

; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MJU-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIORITY NUMBER: 60/542,357
; PRIORITY FILING DATE: 2004-02-06
; PRIORITY APPLICATION NUMBER: 60/613,854
; PRIORITY FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-60

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Query Match 93.9%; Score 524; DB 11; Length 128;
Best Local Similarity 94.4%; Pred. No. 1e-36;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 BIVLTQSPGTLISPGERATLSCASQSSSYLAWQQXPQGQAPRLLIYATSSRATGIP 60
Qy 21 EIVLTQSPGTLISPGERATLSCASQSSSYLAWQQXPQGQAPRLLIYATSSRATGIP 80
Db 61 DRFSGSGSGTDFLTISRLPEPDAVYYCQQYGSSPCSFGQGTKLBIK 108
Db 81 DRFSGSGSGTDFLTISRLPEPDAVYYCQQYGSSTWFQGTVKBIK 128

RESULT 13
US-11-211-917-113
; Sequence 113, Application US/11211917
; Publication No. US2006009360A1
; GENERAL INFORMATION.
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABK-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 108
; TYPE: PPT
; ORGANISM: Homo sapiens
US-11-211-917-113

Query Match 93.7%; Score 523; DB 10; Length 108;
Best Local Similarity 93.5%; Pred. No. 1.1e-36;
Matches 101; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
;

Qy 1 BIVLTQSPGTLISPGERATLSCASQSSSYLAWQQXPQGQAPRLLIYATSSRATGIP 60
Qy 21 EIVLTQSPGTLISPGERATLSCASQSSSYLAWQQXPQGQAPRLLIYATSSRATGIP 60
Db 61 DRFSGSGSGTDFLTISRLPEPDAVYYCQQYGSSPCSFGQGTKLBIK 108
Db 81 DRFSGSGSGTDFLTISRLPEPDAVYYCQQYGSSTWFQGTVKBIK 108

RESULT 14
US-11-128-900-14
; Sequence 14, Application US/1128900
; Publication No. US20050287136A1
; GENERAL INFORMATION.
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVBU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABK-PF/1 DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR APPLICATION NUMBER: US 09/472087

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PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: US 60/113647
 PRIOR FILING DATE: 1998-12-23
 NUMBER OF SEQ ID NOS: 147
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 14
 LENGTH: 235
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-128-900-14

Query Match 93.4%; Score 521; DB 11; Length 235;
 Best Local Similarity 91.7%; Pred. No. 3.1e-36;
 Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKRGQAPRLIYATSSRATGIP 60
 Db 21 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKRGQAPRLIYATSSRATGIP 80
 Qy 61 DRFGSGSGTDFTLTISRLPEPDFAVYCCOYGSPPCSFGGTKEIK 108
 Db 81 DRFGSGSGTDFTLTISRLPEPDFAVYCCOYGSPPCSFGGTKEIK 128

RESULT 15
 US-11-128-900-65
 Sequence 65, Application US/11128900
 Publication No. US20050287136A1
 GENERAL INFORMATION:
 APPLICANT: HANSON, DOUGLAS C.
 APPLICANT: NEVEU, MARK J.
 APPLICANT: MUELLER, EILEEN E.
 APPLICANT: HANKE, JEFFREY H.
 APPLICANT: GILMAN, STEVEN C.
 APPLICANT: DAVIS, C. GEOFFREY
 APPLICANT: CORVALAN, JOSE R.
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
 FILE REFERENCE: ABX-PF1.DIV3
 CURRENT APPLICATION NUMBER: US/11/129,900
 CURRENT FILING DATE: 2005-05-12
 PRIOR APPLICATION NUMBER: US 10/776649
 PRIOR FILING DATE: 2004-02-10
 PRIOR APPLICATION NUMBER: US 10/612497
 PRIOR APPLICATION NUMBER: 2003-07-01
 PRIOR APPLICATION NUMBER: US 09/472087
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: US 60/113647
 PRIOR FILING DATE: 1998-12-23
 NUMBER OF SEQ ID NOS: 147
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 65
 LENGTH: 235
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-128-900-65

Query Match 93.4%; Score 521; DB 11; Length 235;
 Best Local Similarity 91.7%; Pred. No. 3.1e-36;
 Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKRGQAPRLIYATSSRATGIP 60
 Db 21 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAWYQKRGQAPRLIYATSSRATGIP 80
 Qy 61 DRFGSGSGTDFTLTISRLPEPDFAVYCCOYGSPPCSFGGTKEIK 108
 Db 81 DRFGSGSGTDFTLTISRLPEPDFAVYCCOYGSPPCSFGGTKEIK 128

Result No.	Score	Query	Match	Length	DB	ID	Description
1	535	95.9	108	2	C30608		Ig kappa chain V-I
2	535	95.9	109	2	H30601		Ig kappa chain V-I
3	534	95.7	109	2	F30601		Ig kappa chain V-I
4	533	95.5	109	2	B30601		Ig kappa chain V-I
5	531	95.2	109	2	PH0963		Ig kappa chain V-I
6	531	95.2	109	2	D30601		Ig kappa chain V-I
7	530	95.0	109	2	C30601		Ig kappa chain V-I
8	530	95.0	129	2	S43369		IG light chain var
9	529	94.8	134	2	S38643		Ig kappa chain V-I
10	529	94.8	109	2	G30601		Ig kappa chain V-I
11	529	94.8	129	2	G4532		anti-Sm antibody V
12	528	94.6	129	1	K3H01A		Ig kappa chain pre
13	527	94.4	128	1	S20636		Ig kappa chain V-I
14	526	94.3	129	1	K3H01H		Ig kappa chain pre
15	524	93.9	109	1	K3H01T		Ig kappa chain V-I
16	524	93.9	109	1	F30607		Ig kappa chain V-I
17	523.5	93.8	114	2	S46307		Ig kappa chain V-J
18	521	93.4	109	1	K3H01I		Ig kappa chain V-I
19	520	93.2	109	2	A30608		Ig kappa chain V-I
20	515	92.3	109	2	G30607		Ig kappa chain V-I
21	514	92.1	107	2	PH0965		Ig kappa chain V-I
22	514	92.1	108	2	B30608		Ig kappa chain V-I
23	513	91.9	124	2	S20633		Ig kappa chain - h
24	511	91.6	121	2	S4327		Ig kappa chain V-I
25	508	91.0	109	1	K3H01W		Ig kappa chain V-I
26	507	90.9	110	2	S20635		Ig kappa chain V-I
27	505.5	90.4	108	2	E30609		Ig kappa chain V-I
28	505.5	90.2	110	2	E30607		Ig kappa chain V-I
29	503	90.1	108	1	K3H01		Ig kappa chain V-I

C; Superfamily: immunoglobulin V region; immunoglobulin homology
 C; Keywords: heterotramer; immunoglobulin <IMM>
 P; 16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 535; DB 2; Length 109;
 Best Local Similarity 96.3%; Pred. No. 3. 8e-38;
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSYLAQKPGQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSYLAQKPGQAPRLIYASSRATGIP 60

Qy 61 DRFGSGSGTDEFTLTLISRLPEDFAVYQCGYSSPCSFQGQTKLEIK 108
 Db 61 DRFGSGSGTDEFTLTLISRLPEDFAVYQCGYSSPCSFQGQTKLEIK 108

RESULT 3
 P30601 Ig kappa chain V-III region (Neu) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C;Accession: F30601
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
 J; Immunol. 142, 3158-3163, 1989
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
 A;Reference number: A30601; MUID:89215279; PMID:2496160
 A;Accession: F30601
 A;Status: preliminary
 A;Molecule type: protein
 A;Cross-references: UNIPARC:UPI0000176AE9
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 P;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 534; DB 2; Length 109;
 Best Local Similarity 93.5%; Pred. No. 4. 6e-38;
 Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSYLAQKPGQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSYLAQKPGQAPRLIYASSRATGIP 60

Qy 61 DRFGSGSGTDEFTLTLISRLPEDFAVYQCGYSSPCSFQGQTKLEIK 108
 Db 61 DRFGSGSGTDEFTLTLISRLPEDFAVYQCGYSSPCSFQGQTKLEIK 108

RESULT 6
 D30601 Ig kappa chain V-III region (Cur) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
 C;Accession: D30601
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
 J; Immunol. 142, 3158-3163, 1989
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
 A;Reference number: A30601; MUID:89215279; PMID:2496160
 A;Accession: D30601
 A;Status: preliminary
 A;Molecule type: protein
 A;Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE9
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 P;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.2%; Score 531; DB 2; Length 109;
 Best Local Similarity 95.4%; Pred. No. 5. 6e-38;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSYLAQKPGQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSYLAQKPGQAPRLIYASSRATGIP 60

RESULT 4
 B30601 Ig kappa chain V-III region (Glo) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
 C;Accession: B30601
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo
 J; Immunol. 142, 3158-3163, 1989
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
 A;Reference number: A30601; MUID:89215279; PMID:2496160
 A;Accession: B30601
 A;Status: preliminary
 A;Molecule type: protein
 A;Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE7
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 P;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.5%; Score 533; DB 2; Length 109;
 Best Local Similarity 95.4%; Pred. No. 5. 6e-38;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSYLAQKPGQAPRLIYATSSRATGIP 60

Qy 61 DRFGSGSGGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108
 Db 61 DRFGSGSGGTDTPLTISRLPEDFAVYCCQGSSPCSGQGTTKVEIK 108

RESULT 7
 C30601 19 kappa chain V-III region (Pay) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
 C;Accession: C30601
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Carson, D.; Soldi, J.; Immunol. 142, 3158-3163, 1989
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
 A;Reference number: A30601; MUID:89215279; PMID:2496160
 A;Accession: C30601
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-109 <GEN>
 A;Cross-references: UNIPROT:Q9UJ78; UNIPARC:UPI0000176AEB
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 134;
 Best Local Similarity 95.4%; Pred. No. 1.2e-37;
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSYLLWYQKPGQAPRLIYATSSRATGIP 60
 Db 1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSYLLWYQKPGQAPRLIYCASSRATGIP 60

Qy 61 DRFGSGSGGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108
 Db 61 DRFGSGSGGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKVEIK 108

RESULT 8
 S46369 Ig light chain variable region (VJ) - human
 C;Species: Homo sapiens (man)
 C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C;Accession: S46369
 R;Benimoin, C.; Chastagner, P.; Zouali, M.
 EMBOL J. 13, 2951-2962, 1994
 A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement
 A;Reference number: S46369; MUID:94313975; PMID:8039491
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-129 <GEN>
 A;Cross-references: UNIPARC:UPI0000176CA5; EMBL:227170
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 129;
 Best Local Similarity 95.4%; Pred. No. 1.2e-37;
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSYLLWYQKPGQAPRLIYATSSRATGIP 60
 Db 21 BIVLTQSPGTLSLSPGERATLSCRASQSVSSYLLWYQKPGQAPRLIYCASSRATGIP 80

Qy 61 DRFGSGSGGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKLEIK 108
 Db 81 DRFGSGSGGTDTPLTISRLPEDFAVYCCQYGSSPCSGQGTTKVEIK 128

RESULT 9
 S38643 Ig kappa chain V region - human (fragment)
 C;Species: Homo sapiens (man)

A;Residues: 1-129 <MAH>
 A;Cross-references: UNIPARC:UPT00001166FC; EMBL:246345; NID:9560843; PIDN:CAA86464.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 P;36-111.Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 529; DB 2; Length 129;
 Best Local Similarity 95.4%; Pred. No. 1.4e-37;
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAVYQKPGQAPRLIYATSSRATGIP 60
 Db 21 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAVYQKPGQAPRLIYATSSRATGIP 80

Qy 61 DRFGSGSGGTDTFLTISRLPEPDFAVYCCQYGSSPCSFGQGTKLBIK 108
 Db 81 DRFGSGSGGTDTFLTISRLPEPDFAVYCCQYGSSPCSFGQGTKLBIK 128

RESULT 12
 K3HUTI
 Ig kappa chain precursor V-III region (Hah) - human
 C;Species: Homo sapiens (man)
 C;Accession: PL0022
 C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
 R;KIPPS, T.J.; Tomhave, B.; Chen, P.P.; Carson, D.A.
 J;Exp. Med. 167, 840-852, 1988
 A;Reference number: PL0022
 A;Accession: PL0022
 A;Molecule type: mRNA
 A;Residues: 1-129 <KIP>
 A;Cross-references: UNIPROT:PI18135; UNIPARC:UPI000012E163
 C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
 C;Genetics:
 A;Gene: IGKV3
 A;Cross references: GDB:IGKV3
 A;Map Position: 2p12-2p11
 A;Map Position: 2p12-2p11
 C;Keywords: autoantibody; kappa light chain variable region gene expressed in ch
 P;1-20/Domain: signal sequence #status predicted <SIG>
 P;21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>
 P;21-117/Region: V segment
 P;36-111/Domain: immunoglobulin homology <IMM>
 P;44-55/Region: complementarity-determining 1
 P;71-117/Region: complementarity-determining 2
 P;110-117/Region: complementarity-determining 3
 P;118-129/Region: J segment (JK1)
 P;43-109/Disulfide bonds: #status predicted

Query Match 94.6%; Score 528; DB 1; Length 129;
 Best Local Similarity 94.4%; Pred. No. 1.7e-37;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAVYQKPGQAPRLIYATSSRATGIP 60
 Db 21 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAVYQKPGQAPRLIYATSSRATGIP 80

Qy 61 DRFGSGSGGTDTFLTISRLPEPDFAVYCCQYGSSPCSFGQGTKLBIK 108
 Db 81 DRFGSGSGGTDTFLTISRLPEPDFAVYCCQYGSSPCSFGQGTKLBIK 128

RESULT 13
 S20636
 Ig kappa chain V region - human
 C;Species: Homo sapiens (man)
 C;Accession: S20636
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 R;Lee, S.X.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
 Submitted to the EMBL Data Library, April 1992
 A;Reference number: S20631

A;Accession: S20636
 A;Cross-references: UNIPARC:UPT00001163DC; EMBL:211894; NID:933200; PIDN:CAA77948.1; PID
 A;Molecule type: mRNA
 A;Residues: 1-128 <LRE>
 A;Cross-references: UNIPARC:UPI00001163DC; EMBL:211894; NID:933200; PIDN:CAA77948.1; PID
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin V region; immunoglobulin homology <IMM>
 P;36-111/Domain: immunoglobulin homology <IMM>

Query Match 94.4%; Score 527; DB 2; Length 128;
 Best Local Similarity 94.4%; Pred. No. 2.1e-37;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAVYQKPGQAPRLIYATSSRATGIP 60
 Db 21 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAVYQKPGQAPRLIYATSSRATGIP 80

Qy 61 DRFGSGSGGTDTFLTISRLPEPDFAVYCCQYGSSPCSFGQGTKLBIK 108
 Db 81 DRFGSGSGGTDTFLTISRLPEPDFAVYCCQYGSSPCSFGQGTKLBIK 128

RESULT 14
 K3HUTI
 Ig kappa chain precursor V-III region (Hic) - human
 C;Species: Homo sapiens (man)
 C;Accession: PL0021
 C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
 R;KIPPS, T.J.; Tomhave, B.; Chen, P.P.; Carson, D.A.
 J;Exp. Med. 167, 840-852, 1988
 A;Title: Autoantibody-associated kappa light chain variable region gene expressed in ch
 A;Reference number: PL0021; PMID:88171307; PMID:3127527
 A;Accession: PL0021
 A;Molecule type: mRNA
 A;Cross-references: UNIPROT:PI18136; UNIPARC:UPI000012E164
 C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
 C;Genetics:
 A;Gene: GDB:IGKV3
 A;Cross references: GDB:IGKV3
 A;Map Position: 2p12-2p11
 A;Map Position: 2p12-2p11
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) chains
 C;Keywords: immunoglobulin V region; immunoglobulin homology
 P;1-20/Domain: signal sequence #status predicted <SIG>
 P;21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
 P;21-117/Region: V segment
 P;36-111/Domain: immunoglobulin homology <IMM>
 P;44-55/Region: complementarity-determining 1
 P;71-117/Region: complementarity-determining 2
 P;110-117/Region: complementarity-determining 3
 P;118-129/Region: J segment (JK1)
 P;43-109/Disulfide bonds: #status predicted

Query Match 94.3%; Score 526; DB 1; Length 129;
 Best Local Similarity 94.4%; Pred. No. 2.5e-37;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAVYQKPGQAPRLIYATSSRATGIP 60
 Db 21 BIVLTQSPGTLSLSPGERATLSCRASQVSSESYLAVYQKPGQAPRLIYATSSRATGIP 80

Qy 61 DRFGSGSGGTDTFLTISRLPEPDFAVYCCQYGSSPCSFGQGTKLBIK 108
 Db 81 DRFGSGSGGTDTFLTISRLPEPDFAVYCCQYGSSPCSFGQGTKLBIK 128

RESULT 15
 K3HUTI
 Ig kappa chain V-III region (Ti) - human
 C;Species: Homo sapiens (man)
 C;Accession: S20636
 C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C;Accession: A01895
 R;Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
 A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
 A;Reference number: A91651; MUID:72188439; PMID:5027703
 A;Accession: A01895
 A;Molecule type: protein
 A;Residues: 1-109 ^Y
 A;Cross-references: UNIPROT:P01622; UNIPARC:UPI000012E15D
 A;Note: the sequence of the C region, which has the Inv (3) marker, is also given
 C;Comment: This is a Bence Jones protein.
 C;Genetics:
 A;Gene: GDB:IGKV3
 A;Map position: 2p12-2p11
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer
 P;16-91/Domain: immunoglobulin homology <IMM>
 P;23-89/Disulfide bonds: #status predicted

Query Match 93.9%; Score 524; DB 1; Length 109;
 Best Local Similarity 92.6%; Pred. No. 3.2e-37;
 Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 EIVLTQSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKKGQAPPLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASOSVNSFLAWYQQKKGQAPPLIYASSSRATGIP 60
 Qy 61 DRFGSGSGGTDFPLTISRLPEPDFAVYCCOOGSSPCSGCQGKLEIK 108
 Db 61 DRFGSGSGGTDFPLTISRLPEPDFAVYCCQGSSPFGQGKLEIK 108

Search completed: May 15, 2006, 17:04:49
 Job time : 22.7854 secs

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OX	FT	NON_TER	108	108	AA;	11636	MW;	8BC14FF07A419E3D	CRC64;
RN	SQ	SEQUENCE	108	AA.					
[1]	NUCLEOTIDE SEQUENCE.								
RX	Medline=8277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;								
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,								
RA	Young D.C.;								
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal								
RT	fetus."								
RL	Clin. Immunol. Immunopathol. 87:184-192 (1998).								
DR	IPR007110; ADD6264.1; - mRNA.								
DR	EMBL:AF03028; B30607; B30607.								
DR	PIR; I30601; I30601.								
DR	HSSP; P01625; 1Bx3.								
SNR	Q9UL86; 1-109.								
DR	Ensembl; ENSG0000169769; Homo sapiens.								
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003556; Ig_v.								
DR	SMART; SM00406; IgV; 1.								
PROSIT	PS00835; Ig_LIKE; 1.								
FT	NON_TER	1							
FT	NON_TER	109	109	AA;	11928	MW;	24332872727DAC83	CRC64;	
SQ	SEQUENCE	109	AA;	11928	MW;	24332872727DAC83	CRC64;		
Query	Match	90.3%	Score	504;	DB 2;	Length	109;		
Db	Best Local Similarity	91.7%;	Pred.	No. 1..8e-44;					
Matches	99;	Conservative	3;	Mismatches	6;	Indels	0;	Gaps	0;
Query	1	EIVLTQSPGTLSLSPGERATLSRASQVSSYIAYQQKPGQAPRILIVATSRATGIP	60						
Db	1	EIVLTQSPGTLSLSPGERATLSRASQVSSYIAYQQKPGQAPRILIVATSRATGIP	60						
Query	61	DRFGSGSGTDFLTISRLPEDFAVYTCQQYGSPPSFQGTKEIK	108						
Db	61	DRFGSGSGTDFLTISRLPEDFAVYTCQQYGSPPSFQGTKEIK	108						
RESULT	9								
KV3A_HUMAN	ID	KV3A_HUMAN	STANDARD;		PRT;	108	AA.		
AC	P01619.								
AC	21-JUL-1986 (Rel. 01, Created)								
DT	21-JUL-1986 (Rel. 01, Last sequence update)								
DT	10-MAY-2005 (Rel. 47, Last annotation update)								
DE	19 kappa chain V-III region B6.								
OS	Homo sapiens (Human).								
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Buarchoontoglires; Primates; Catarrhini; Hominidae;								
RN	[1]	NCBI_TaxID=9606;							
RP	PROTEIN SEQUENCE.								
RX	PubMed:11945339;								
RA	Milstein C.;								
RT	"The basic sequences of immunoglobulin kappa chains: sequence studies of Bence Jones proteins Rad, F4 and B6."								
RL	FEBS Lett. 2:301-304 (1969).								
CC	-1 - MISCELLANEOUS: This is a Bence-Jones protein.								
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.								
DR	A01891; K3HUGO.								
DR	HSSP; P01625; 1BxQ.								
DR	InterPro; IPR007110; Ig-1like.								
DR	SMART; SM00406; IgV; 1.								
DR	PROSIT; PS00835; Ig_LIKE; 1.								
KW	Direct protein sequencing; Immunoglobulin domain;								
KW	Immunoglobulin V region.								
FT	DISULFD	23	89	AA;	11830	MW;	9319A5B1D93588B6	CRC64;	
SQ	SEQUENCE	109	AA;	11830	MW;	9319A5B1D93588B6	CRC64;		
Query	Match	89.6%	Score	500;	DB 1;	Length	109;		
Db	Best Local Similarity	89.8%;	Pred.	No. 4.6e-44;					
Matches	97;	Conservative	3;	Mismatches	8;	Indels	0;	Gaps	0;
Query	1	EIVLTQSPGTLSLSPGERATLSRASQVSSYIAYQQKPGQAPRILIVATSRATGIP	60						
Db	1	EIVLTQSPGTLSLSPGERATLSRASQVSSYIAYQQKPGQAPRILIVATSRATGIP	60						
Query	61	DRFGSGSGTDFLTISRLPEDFAVYTCQQYGSPPSFQGTKEIK	108						
Db	61	DRFGSGSGTDFLTISRLPEDFAVYTCQQYGSPPSFQGTKEIK	108						
FT	DISULFD	23	89	AA;	11830	MW;	9319A5B1D93588B6	CRC64;	

RESULT 11	Q6PF2_HUMAN PRELIMINARY;	PRT;	235 AA.					
ID	Q6PF2;							
AC	Q6PF2;							
DT	05-JUL-2004 (TREMBrel. 27, Created)							
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)							
DT	05-JUL-2004 (TREMBrel. 27, Last annotation update)							
DE	Hypothetical protein.							
OS	Homo sapiens (Human);							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
OX	NCBI_TaxID=9606;							
RN								
RP	NUCLEOTIDE SEQUENCE.							
RC	TISSUE=Lung;							
RX	Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;							
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Degege J.G.,							
RA	Klaunser R.D., Collins F.S., Wagner L., Shevchenko C.M., Schulter G.D.,							
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P.,							
RA	Hopkins N.K., Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.P.,							
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,							
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,							
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,							
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,							
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,							
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,							
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Soderberg E.J., Liu X., Gibbs R.A.,							
RA	Villalon D.K., Muzny D.M., Soderberg E.J., Liu X., Gibbs R.A.,							
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,							
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,							
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,							
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,							
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,							
RA	Schnerr A., Schein J.E., Jones S.J.M., Marra M.A.,							
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";							
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";							
RL	proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).							
RN								
RP	NUCLEOTIDE SEQUENCE.							
RC	TISSUE=Spleen;							
RA	Strausberg R.J.							
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.							
DR	EMBL; BC016380; AAH16380.1; -; mRNA.							
DR	HSSP; P01837; 1KCU.							
DR	SMART; Q6PF2;	21-235						
DR	InterPro; IPR003599; Ig-							
DR	InterPro; IPR007110; Ig-like.							
DR	InterPro; IPR003597; Ig-cl.							
DR	InterPro; IPR003097; Ig-MHC.							
DR	InterPro; IPR003096; Ig-V.							
DR	InterPro; IPR003596; Ig-Y.							
DR	Pfam; PF07654; Cl-set; 1.							
DR	SMART; SM00409; Ig; 2.							
DR	SMART; SM00407; IgCl1.							
DR	SMART; SM0046; IgV; 1.							
DR	PROSITE; PS50835; Ig_LIKE; 2.							
DR	PROSITE; PS000290; Ig_MHC; UNKNOWN_1.							
KW	Hypothetical protein.							
SQ	SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;							
Query Match	88.4%; Score 493; DB 2; Length 235;							
Best Local Similarity	88.0%; Pred. No. 6e-43; Indels 0; Gaps 0;							
Matches	95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;							
Qy	1 EIVLTQSPGTLSLSPGERATLSCRSQVSSEYLVQKQGQAPLLIYATSSRATGIP 60							
Db	21 EIVLTQSPGTLSLSPGERATLSCRSQVSSEYLVQKQGQAPLLIYATSSRATGIP 80							
Qy	61 DRFGSGSSGTTGTTLSLSPGERATLSCRSQVSSEYLVQKQGQAPLLIYATSSRATGIP 108							
Db	81 DRFGSGSSGTTGTTLSLSPGERATLSCRSQVSSEYLVQKQGQAPLLIYATSSRATGIP 128							
	RESULT 13							
	Q6PS88_HUMAN							

ID	Q6P5SB_HUMAN PRELIMINARY;	ERT;	236 AA.	AC	P01621;	DT	21-JUL-1986 (Rel. 01, Created)
DR	Q6P5SB;					DT	21-JUL-1986 (Rel. 01, Last sequence update)
DR	05-JUL-2004 (TREMBLrel. 27, Created)					DT	10-MAY-2005 (Rel. 47, Last annotation update)
DR	05-JUL-2004 (TREMBLrel. 27, Last sequence update)					DT	10-MAY-2005 (Rel. 47, Last annotation update)
DB	Hypothetical protein.					DS	Ig kappa chain V-III region NG9 precursor (fragment).
OS	Homo sapiens (Human).					OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OC						OC	
OC						OC	
OX	NCBI_TAXID=9606;					OX	NCBI_TAXID=9606;
RN						RN	[1]
RP						RP	
RC	NUCLEOTIDE SEQUENCE.					RC	
RC	TISSUE-Glandular pool- thyroid;					RC	
RC	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;					RC	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					RA	Bentley D.L./
RA	Klaunser R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,					RA	"Most kappa immunoglobulin mRNA in human lymphocytes is homologous to a small family of germ-line V genes.";
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					RA	RT
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					RA	RT
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					RA	RT
RA	Stapleton M., Soares M.B., Bonaido M.P., Casavant T.L., Scheetz T.E.,					RA	RT
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,					RA	RT
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,					RA	RT
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					RA	RT
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					RA	RT
RA	Villanova D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					RA	RT
RA	Fahey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,					RA	RT
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					RA	RT
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					RA	RT
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					RA	RT
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,					RA	RT
RA	Schnecher A., Schein J.E., Jones S.J.M., Marra M.A.,					RA	RT
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";					RT	RT
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).					RT	RT
RL						RL	
RN						RN	
RC	NUCLEOTIDE SEQUENCE.					RC	
RC	TISSUE-Glandular pool- thyroid;					RC	
RA	Strausberg R.;					RA	
RA	Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.					RA	
DR	EMBL; BC062704; AAH62704.1; - mRNA.					DR	
DR	HSSP; P01837; IKGU.					DR	
DR	Q6P5SB; Q6PS835; 21-236.					DR	
DR	InterPro; IPR003599; Ig.					DR	
DR	InterPro; IPR007110; Ig-like.					DR	
DR	InterPro; IPR00597; Ig_C1.					DR	
DR	InterPro; IPR003006; Ig_MHC.					DR	
DR	PFAM; PF07654; C1-set; 1.					DR	
DR	SMART; SM00409; Ig; 2.					DR	
DR	SMART; SM00407; IgC1.					DR	
DR	SMART; SM00406; IgV; 1.					DR	
DR	SMART; PS50835; Ig_LIKE; 2.					DR	
DR	PROSITE; PS010290; Ig_MHC; UNKNOWN_1.					DR	
KW	Hypothetical protein.					KW	
SEQUENCE	236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;					SEQUENCE	
Query	Best Local Similarity 86.3%; Score 481.5%; DB 2; Length 236;					Query	RESULT 15
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3K_HUMAN
Db	1 BIVLTQSPGTLSLSPGERATLSCRASQVSSESSLYANTQKQPCQAPRLIYATSSRATGIP 60					Db	ID KV3K_HUMAN
Db	21 BIVLTQSPGTLSFSPGERATLSCRASQTVFSSHLANTQKQPCQAPRLIYAGGSRATGIP 80					Db	STANDARD;
Qy	61 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGSPP-CSFGGGTKEIK 108					Qy	PRT;
Db	65 DRFGSGASGTDFTLTSRLEPDFAVYQQYGSNS 99					Db	128 AA.
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129					Db	ID KV3C_HUMAN
Qy	Best Local Similarity 85.3%; Score 481.5%; DB 2; Length 236;					Qy	RESULTS 14
Matches	93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;					Matches	KV3C_HUMAN
Db	81 DRFGSGGGTGTDFLTLSRLEPDFAVYQQYGTSPSLTGGTRVIK 129						

RA Klöbeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.,
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 RT III.";
 RL Nucleic Acids Res. 13:6489-6513 (1985).

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CC
 DR EMBL; 200021; CRA77316.1; -; Genomic_DNA.
 DR PIR; A01893; K3HU41.
 DR HSSP; P01625; 1EEQ.
 DR SMR; P06311; 21-128.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 PT SIGNAL 1 20 Ig kappa chain V-III region IARC/BL41.
 PT CHAIN 21 128 Framework-1.
 PT REGION 21 43 Complementarity-determining-1.
 PT REGION 44 54 Framework-2.
 PT REGION 55 69 Complementarity-determining-2.
 PT REGION 70 76 Framework-3.
 PT REGION 77 108 Complementarity-determining-3.
 PT REGION 109 117 JK1 segment.
 PT REGION 118 128 By similarity.
 PT DISUFD 43 108 By similarity.
 PT NON_TER 128 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;
 SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;
 Query Match 83.4%; Score 465.5; DB 1; Length 128;
 Best Local Similarity 87.0%; Pred. No. 2.1e-40;
 Matches 94; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
 Qy 1 EIVLTOSPGTLSLSPGERATLSCRASQVSSSYLVYQKQEPQAPRLIYATSSRATGIP 60
 Db 21 EIVLTOSPGTLSLSPGERATLSCRASQVSSSYLVYQKQEPQAPRLIYATSSRATGIP 79
 Qy 61 DRRSGSGSGTGTDTLTLISRLPEDPEAIVY CQYQGSSSPCSFGQGTKEIK 108
 Db 80 DRFGSGSGTGTDTLTLISRLPEDPEAIVY CQYQYTSPTYFGQGTKEIK 127

Search completed: May 15, 2006, 17:03:56
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